

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:31:40 ; Search time 7.32042 Seconds

(without alignments)  
612.211 Million cell updates/sec

Title: US-09-728-911-2

Perfect score: 1244

Sequence: 1 MMRKCFGLFSLFGLTGVVA.....YQPMDDRQRSSERCVEIP 231

Scoring table: BLOSUM62  
Gap 10.0, Gapext 0.5

Searched: 118974 seqs, 19401057 residues  
T number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/prodata/1/pubpaa/PC7\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 5: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 6: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 8: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/prodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1244	100.0	231	10	US-09-728-911-2
2	1244	100.0	231	10	US-09-949-192-6
3	1130	90.8	210	10	US-09-728-911-13
4	336	27.0	207	10	US-09-746-359A-65
5	336	27.0	214	10	US-09-746-359A-63
6	336	27.0	217	10	US-09-746-359A-55
7	336	27.0	221	10	US-09-746-359A-12
8	336	27.0	542	9	US-10-028-072-188
9	336	27.0	542	12	US-10-052-586-398
10	336	27.0	547	10	US-09-746-359A-54
11	336	27.0	553	10	US-09-746-359A-11
12	336	27.0	553	10	US-09-949-192-7
13	336	27.0	559	10	US-09-746-359A-62
14	336	27.0	571	10	US-09-746-359A-53
15	336	27.0	594	10	US-09-746-359A-23
16	302	24.3	217	10	US-09-746-359A-38
17	302	24.3	514	10	US-09-746-359A-39
18	302	24.3	546	10	US-09-746-359A-37
19	289	23.2	56	10	US-09-864-761-40289

20	289	23.2	56	10	US-09-864-761-47623	Sequence 47623, A
21	266	21.4	574	9	US-09-912-672A-2	Sequence 2, App1
22	266	21.4	574	10	US-10-063-547-164	Sequence 164, App
23	266	21.4	574	10	US-09-728-911-25	Sequence 25, App1
24	266	21.4	574	10	US-09-870-574-4	Sequence 4, App1
25	266	21.4	574	12	US-10-006-867-164	Sequence 164, App
26	263	21.1	211	10	US-09-728-911-34	Sequence 34, App1
27	263	21.1	212	9	US-09-912-672A-5	Sequence 6, App1
28	263	21.1	560	9	US-09-912-672A-6	Sequence 6, App1
29	211	17.0	150	10	US-09-746-359A-56	Sequence 23, App1
30	174.5	14.0	308	9	US-09-912-672A-23	Sequence 20, App1
31	172	13.8	295	10	US-09-103-067-20	Sequence 3, App1
32	172	13.8	295	10	US-09-949-192-3	Sequence 3, App1
33	168.5	13.5	199	10	US-09-728-911-35	Sequence 35, App1
34	168.5	13.5	325	9	US-10-066-800-137	Sequence 137, App
35	168.5	13.5	325	10	US-09-870-574-3	Sequence 3, App1
36	168.5	13.5	325	10	US-09-949-192-5	Sequence 5, App1
37	168.5	13.5	325	10	US-09-949-192-5	Sequence 390, App
38	164.5	13.2	196	10	US-09-052-586-390	Sequence 67, App1
39	164.5	13.2	201	9	US-09-912-672A-16	Sequence 16, App1
40	164.5	13.2	201	10	US-09-746-359A-59	Sequence 59, App1
41	164.5	13.2	203	10	US-09-746-359A-15	Sequence 15, App1
42	164.5	13.2	219	10	US-09-355-000-7	Sequence 7, App1
43	164.5	13.2	282	9	US-09-912-672A-15	Sequence 15, App1
44	164.5	13.2	307	10	US-09-746-359A-58	Sequence 58, App1
45	164.5	13.2	311	9	US-09-978-295A-352	Sequence 352, App

## ALIGNMENTS

RESULT 1  
US-09-728-911-2  
Sequence 2, Application US/09728911  
Parent No. US2002012669A1  
GENERAL INFORMATION:  
APPLICANT: Presnell, Scott R.  
APPLICANT: Xu, Wenfeng  
APPLICANT: Kindvogel, Wayne  
APPLICANT: Chen, Zhi  
TITLE OF INVENTION: Human Cytokine Receptor  
FILE REFERENCE: 99-93  
CURRENT APPLICATION NUMBER: US/09/728,911  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US 60/169,049  
PRIOR FILING DATE: 1999-12-03  
PRIOR APPLICATION NUMBER: US 60/232,219  
PRIOR FILING DATE: 2000-09-13  
PRIOR APPLICATION NUMBER: US 60/244,610  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 231  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-728-911-2

Query Match 100.0%; Score 1244; DB 10; Length 231;  
Best Local Similarity 100.0%; Pred. No. 8.3e-115;  
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMRKCFGLFSLFGLTGVVA.....YQPMDDRQRSSERCVEIP 60  
DB 1 MMRKCFGLFSLFGLTGVVA.....YQPMDDRQRSSERCVEIP 60  
QY 61 FVQYKYGORWKNKEDCGTOELSCDLTSETSDIOEYFVRVAASAGSYSESMPTRF 120  
DB 61 FVQYKYGORWKNKEDCGTOELSCDLTSETSDIOEYFVRVAASAGSYSESMPTRF 120  
QY 121 TPWWEKIDPVMNITGVNGLVTLHA PNL PYRQKEKNVSIIDYVELLYRVTIINSL 180  
DB 121 TPWWEKIDPVMNITGVNGLVTLHA PNL PYRQKEKNVSIIDYVELLYRVTIINSL 180

Qy 181 EKEQYVEGAHRAVEIALTPHSSYCVVAEIQPMLDRRSQSEERCVIEP 231  
 Db 181 EKEQYVEGAHRAVEIALTPHSSYCVVAEIQPMLDRRSQSEERCVIEP 231

RESULT 2

US-09-949-192-6  
 ; Sequence 6, Application US/09949192  
 ; Patent No. US20020142292A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Parham, Christi L.  
 ; APPLICANT: Gorman, Daniel L.  
 ; APPLICANT: Kurata, Hirokazu  
 ; APPLICANT: Arai, Naoko  
 ; APPLICANT: Sana, Theodore R.  
 ; APPLICANT: Mattson, Jeanine D.  
 ; APPLICANT: Murphy, Erin E.  
 ; APPLICANT: Savkoor, Chetan  
 ; APPLICANT: Grein, Jeffery  
 ; APPLICANT: Smith, Kathleen M.  
 ; APPLICANT: McManahan, Terrill K.  
 ; TITLE OF INVENTION: MAMMALIAN GENES; RELATED REAGENTS AND METHODS  
 ; FILE REFERENCE: DX01169K  
 ; CURRENT APPLICATION NUMBER: US/09/949,192  
 ; CURRENT FILING DATE: 2001-09-07  
 ; PRIOR APPLICATION NUMBER: 60/231,267  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 53  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 6  
 ; LENGTH: 231  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

Query Match 100.0%; Score 1244; DB 10; Length 231;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-115;  
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPMKCHFLGFLISFFLTGVTAGTQSTHESLKPORVQFQSRNPHNLOQPGRAITGNSVY 60  
 Db 1 MPMKCHFLGFLISFFLTGVTAGTQSTHESLKPORVQFQSRNPHNLOQPGRAITGNSVY 60

Qy 61 FVOYKIYQORQWKNKEDCWGTQELSCDLTSETSDIQEPIYGRVRAAASAGSYSEWMTPRF 120  
 Db 61 FVOYKIYQORQWKNKEDCWGTQELSCDLTSETSDIQEPIYGRVRAAASAGSYSEWMTPRF 120

Qy 121 TPWWTETKIDPPVNNITQVNGSLLVILHAPNLPYRQYQKKNVSIEDYVYLLRVFIINSL 180  
 Db 121 TPWWTETKIDPPVNNITQVNGSLLVILHAPNLPYRQYQKKNVSIEDYVYLLRVFIINSL 180

Qy 181 EKEQYVEGAHRAVEIALTPHSSYCVVAEIQPMLDRRSQSEERCVIEP 231  
 Db 181 EKEQYVEGAHRAVEIALTPHSSYCVVAEIQPMLDRRSQSEERCVIEP 231

RESULT 3  
 US-09-728-911-13  
 ; Sequence 13, Application US/09728911  
 ; Patent No. US20020012669A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Presnell, Scott R.  
 ; APPLICANT: Xu, Wenfeng  
 ; APPLICANT: Kindsvogel, Wayne  
 ; APPLICANT: Chen, Zhi  
 ; TITLE OF INVENTION: Human Cytokine Receptor  
 ; FILE REFERENCE: 99-93  
 ; CURRENT APPLICATION NUMBER: US/09/728,911  
 ; CURRENT FILING DATE: 2000-12-01  
 ; PRIOR APPLICATION NUMBER: US 60/169,049  
 ; PRIOR FILING DATE: 1999-12-03  
 ; PRIOR APPLICATION NUMBER: US 60/232,219

Query Match 27.0%; Score 336; DB 10; Length 207;  
 Best Local Similarity 37.2%; Pred. No. 9.5e-26;  
 Matches 74; Conservative 33; Mismatches 90; Indels 2; Gaps 2;

Qy 30 KPORVQFQSRNPHNLOQPGRAITGNSVYFVQYKIYQORQWKNKEDCWGTQELSCDLT 89  
 Db 3 KPANITFLSINMKVNLQWTPPEGLQGVKVTYVQYFIYQKKNKSECRINRYCDLS 62

Qy 90 SETSDIQEPIYGRVRAAASAGSYSEWMTPRTPWWTETKIDPPVNNITQVNGSLLVILHAP 149

; PRIOR FILING DATE: 2000-09-13  
 ; PRIOR APPLICATION NUMBER: US 60/244,610  
 ; PRIOR FILING DATE: 2000-10-31  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 13  
 ; LENGTH: 210  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-728-911-13

Query Match 90.8%; Score 1130; DB 10; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-103;  
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 TQSTHESLKPORVQFQSRNPHNLOQPGRAITGNSVYFVQYKIYQORQWKNKEDCWGT 81  
 Db 1 TQSTHESLKPORVQFQSRNPHNLOQPGRAITGNSVYFVQYKIYQORQWKNKEDCWGT 60

Qy 82 QELSCDLTSETSDIQEPIYGRVRAAASAGSYSEWMTPRTPWWTETKIDPPVNNITQVNGS 141  
 Db 61 QELSCDLTSETSDIQEPIYGRVRAAASAGSYSEWMTPRTPWWTETKIDPPVNNITQVNGS 120

Qy 142 LLVILHAPNLPYRQYQKKNVSIEDYVYLLRVFIINNSLEKQYVEGAHRAVEIALTP 201  
 Db 121 LLVILHAPNLPYRQYQKKNVSIEDYVYLLRVFIINNSLEKQYVEGAHRAVEIALTP 180

Qy 202 HSSYCVVAEIQPMLDRRSQSEERCVIEP 231  
 Db 181 HSSYCVVAEIQPMLDRRSQSEERCVIEP 210

RESULT 4  
 US-09-746-359A-65  
 ; Sequence 65, Application US/09746359A  
 ; Patent No. US20020042366A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Thompson, Penny  
 ; APPLICANT: Foster, Donald C.  
 ; APPLICANT: Xu, Wenfeng  
 ; APPLICANT: Madden, Karen L.  
 ; APPLICANT: Kelly, James D.  
 ; APPLICANT: Sprecher, Cindy A.  
 ; APPLICANT: Blumberg, Hal  
 ; APPLICANT: Eagan, Maribeth A.  
 ; APPLICANT: Jaspers, Stephen R.  
 ; APPLICANT: Chandrasekhar, Yasmin A.  
 ; APPLICANT: No. US20020042366A1ak, Julia E.  
 ; TITLE OF INVENTION: Method for Treating Inflammation  
 ; FILE REFERENCE: 99-108  
 ; CURRENT APPLICATION NUMBER: US/09/746,359A  
 ; CURRENT FILING DATE: 2001-05-21  
 ; PRIOR APPLICATION NUMBER: 60/171,969  
 ; PRIOR FILING DATE: 1999-12-23  
 ; PRIOR APPLICATION NUMBER: 60/213,341  
 ; PRIOR FILING DATE: 2000-06-22  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 65  
 ; LENGTH: 207  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-746-359A-65

Query Match 27.0%; Score 336; DB 10; Length 207;  
 Best Local Similarity 37.2%; Pred. No. 9.5e-26;  
 Matches 74; Conservative 33; Mismatches 90; Indels 2; Gaps 2;

Qy 30 KPORVQFQSRNPHNLOQPGRAITGNSVYFVQYKIYQORQWKNKEDCWGTQELSCDLT 89  
 Db 3 KPANITFLSINMKVNLQWTPPEGLQGVKVTYVQYFIYQKKNKSECRINRYCDLS 62

Qy 90 SETSDIQEPIYGRVRAAASAGSYSEWMTPRTPWWTETKIDPPVNNITQVNGSLLVILHAP 149

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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:28:46 ; Search time 31.993 Seconds

(without alignments)  
962.115 Million cell updates/sec

Title: US-09-728-911-2

Perfect score: 1244

Sequence: 1 MPMKCFGLFISFLTGVA.....YQMLDRRQSRSERCVEIP 231

Scoring table:

BLOSUM62

Gap 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

908470

Number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

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5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
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22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1244	100.0	231	22	AAE05048
2	1244	100.0	231	22	AAE02460
3	1244	100.0	231	22	AAE02467
4	1244	100.0	231	23	AAO17381
5	1244	100.0	231	23	AAU08000
6	1244	100.0	231	23	ABG34086
7	1244	100.0	231	23	AAE17320
8	1218	97.9	263	23	AAU080324
9	1218	97.9	263	23	AAE17321
10	1214	97.6	263	23	AAO17382

11	1213	97.5	262	22	AAU09186
12	1140	91.6	214	23	AAE17319
13	1130	90.8	210	22	AAE02463
14	1076	86.5	249	22	AAE02458
15	1076	86.5	249	23	AAO17380
16	687	55.2	130	22	AAE02461
17	336	27.0	207	22	AAE05289
18	336	27.0	207	22	ABG67220
19	336	27.0	214	22	AAE05287
20	336	27.0	214	23	ABG67218
21	336	27.0	217	22	AAE05280
22	336	27.0	217	23	ABG67211
23	336	27.0	221	22	AAE05269
24	336	27.0	221	23	ABG67200
25	336	27.0	221	23	AAE23354
26	336	27.0	542	22	AAU02922
27	336	27.0	542	22	AAU12265
28	336	27.0	547	22	AAE05279
29	336	27.0	547	23	ABG67210
30	336	27.0	547	23	AAE23362
31	336	27.0	553	19	AAW79159
32	336	27.0	553	22	ABE11582
33	336	27.0	553	22	AAU04058
34	336	27.0	553	22	AAE05268
35	336	27.0	553	23	ABG67199
36	336	27.0	553	23	AAE23353
37	336	27.0	555	22	AAU04072
38	336	27.0	559	22	AAE05286
39	336	27.0	559	23	AAE23361
40	336	27.0	571	22	AAU04065
41	336	27.0	571	22	AAE05278
42	336	27.0	571	23	ABG67209
43	336	27.0	571	23	AAE23359
44	336	27.0	594	22	AAU04062
45	336	27.0	594	22	AAU04062

## ALIGNMENTS

RESULT 1  
AAE05048  
ID AAE05048 standard; Protein; 231 AA.  
AC AAE05048;  
XX  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Human ZCYTO18 soluble receptor antagonist, zcytor16 protein.  
XX  
XX Human; cytosolic; cytokine; ZCYTO18 protein; genetic abnormality;  
XX cancer; inflammation; gene therapy; zcytor16.  
XX  
XX  
OS Homo sapiens.  
XX  
XX WO200146422-A1.  
XX  
XX 28-JUN-2001.  
XX  
XX PD  
XX PF 22-DEC-2000; 2000MO-US35308.  
XX  
XX PR 23-DEC-1999; 99US-0471767.  
XX PR 01-DEC-2000; 2000US-0250841.  
XX  
XX (ZYMO) ZYMOGENETICS INC.  
XX  
XX PI Presnell SR, Kindsvogel W;  
XX WPI; 2001-408648/43.  
XX DR N-PSDB; AAD09745.  
XX  
XX PT Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer -

PS Example 13A; Page 158-159; 167pp; English.

XX The patent discloses novel human cytokine, ZCYTO18 protein and its

CC corresponding DNA. ZCYTO18 protein induces proliferation of cells

CC expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity

CC in K5626 cells. ZCYTO18 DNA is useful for detecting a genetic

CC abnormality in a patient. ZCYTO18 DNA and its antibodies are useful

CC for detecting cancer and inflammation. ZCYTO18 protein is useful for

CC killing cancer cells. It is useful for increasing platelets in a

CC patient or injured tissue. It is also used in gene therapy.

CC The present sequence is human zcytor16, which is a naturally expressed

CC soluble receptor antagonist of ZCYTO18 protein.

XX Sequence 231 AA;

Query Match 100.0%; Score 1244; DB 22; Length 231;

Best Local Similarity 100.0%; Pred. No. 1.1e-123;

Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPKECFGLISFFLTGVAGTQSTHESLKPORVQFSRNFHNILOWQPGRALTGNSVY 60

DB 1 MNPKECFGLISFFLTGVAGTQSTHESLKPORVQFSRNFHNILOWQPGRALTGNSVY 60

QY 61 FVOYKIYGORQWKNEKDCWGTQELSCDLTSETSDIQEPYGRVRAASAGSYSEWSMTPRF 120

DB 61 FVOYKIYGORQWKNEKDCWGTQELSCDLTSETSDIQEPYGRVRAASAGSYSEWSMTPRF 120

QY 121 TPWETKIDPPVMNITQVNGSLVILHAPNLPYRYQKEKNVSIEDYELLVRFVFIINSL 180

DB 121 TPWETKIDPPVMNITQVNGSLVILHAPNLPYRYQKEKNVSIEDYELLVRFVFIINSL 180

QY 181 EKEQKVEGAHRAVEIEALTTPHSSYCVVAEIIYQPMIDRRSQRSEERCVEIP 231

DB 181 EKEQKVEGAHRAVEIEALTTPHSSYCVVAEIIYQPMIDRRSQRSEERCVEIP 231

RESULT 2

AAE02460

ID AAE02460 standard; Protein; 231 AA.

XX AAE02460;

XX 10-AUG-2001 (first entry)

XX Human DNAX cytokine receptor subunit 4.2 (DCRS4.2).

XX Human; immunomodulator; DNAX cytokine receptor subunit 4.2; DCRS4.2;

KW therapy; immunological disorder; drug screening; cell development;

KW chromosome 6q24.1-25.2.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..21

FT /label= Signal-peptide

FT Protein 22..231

FT /label= DCRS4.2

FT /note= "Human mature DNAX cytokine receptor

FT subunit 4.2"

XX WO200136467-A2.

XX 25-MAY-2001.

XX 16-NOV-2000; 2000WO-US31363.

XX 18-NOV-1999; 99US-0443060.

PR 13-DEC-1999; 99US-0170320.

XX (SCHE ) SCHERING CORP.

XX Gorman DM;

XX

DR WPI; 2001-343800/36.

DR N-PSDB; AAD06414.

XX New mammalian receptor proteins related to cytokine receptors, useful

PT for regulating cell development and for diagnosis and treatment of

FT immunological disorders

XX Claim 3; Page 23; 124pp; English.

XX The present sequence is human DNAX cytokine receptor subunit 4.2

CC (DCRS4.2). DCRS4 gene is located on chromosome 6q24.1-25.2.

CC Cytokine receptors, fragments and antibodies are useful for treating

CC immunological disorders. DCRS3 (50R), DCRS4 (cytor) or fragments are

CC useful in drug screening to identify compounds having binding affinity

CC to the receptor subunit. Modulators of DCRs are useful for modulating

CC the physiology or development of a cell or tissue culture cells. A

CC purified DCRS is useful as a reagent to detect antibodies generated in

CC response to the presence of elevated levels of expression, or

CC immunological disorders which lead to production of antibody to the

CC endogenous receptor. Cytokine receptor sequences are useful as probes

CC for detecting levels of the cytokine receptor in patients suspected of

CC having an immunological disorder. Antibodies have therapeutic value, are

CC useful as potent antagonist, in detecting or quantifying ligands, for

CC isolating DCRS proteins and peptides, to screen expression libraries for

CC particular expression products, to raise anti-idiotypic antibodies and

CC for detecting or diagnosing various immunological conditions related to

CC expression of the protein or cells which express the protein.

XX Sequence 231 AA;

Query Match 100.0%; Score 1244; DB 22; Length 231;

Best Local Similarity 100.0%; Pred. No. 1.1e-123;

Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPKECFGLISFFLTGVAGTQSTHESLKPORVQFSRNFHNILOWQPGRALTGNSVY 60

DB 1 MNPKECFGLISFFLTGVAGTQSTHESLKPORVQFSRNFHNILOWQPGRALTGNSVY 60

QY 61 FVOYKIYGORQWKNEKDCWGTQELSCDLTSETSDIQEPYGRVRAASAGSYSEWSMTPRF 120

DB 61 FVOYKIYGORQWKNEKDCWGTQELSCDLTSETSDIQEPYGRVRAASAGSYSEWSMTPRF 120

QY 121 TPWETKIDPPVMNITQVNGSLVILHAPNLPYRYQKEKNVSIEDYELLVRFVFIINSL 180

DB 121 TPWETKIDPPVMNITQVNGSLVILHAPNLPYRYQKEKNVSIEDYELLVRFVFIINSL 180

QY 181 EKEQKVEGAHRAVEIEALTTPHSSYCVVAEIIYQPMIDRRSQRSEERCVEIP 231

DB 181 EKEQKVEGAHRAVEIEALTTPHSSYCVVAEIIYQPMIDRRSQRSEERCVEIP 231

RESULT 3

AAE02657

ID AAE02657 standard; Protein; 231 AA.

XX AAE02657;

XX 23-JUL-2001 (first entry)

XX Human cytokine receptor, zcytor16.

XX Cytokine receptor; zcytor16; IL-TIF; antiinflammatory; cytostatic;

KW antirheumatic; antiarthritic; antiasthmatic; antiatherosclerotic;

KW immunosuppressive; chromosome 6q24.1-25.2; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 22..108

FT /note= "Ig domain 1"

FT Domain 22..231

FT /note= "extracellular domain"

FT Domain 112..210

/note= "Ig domain 2"

FT WO200140467-A1.  
 XX 07-JUN-2001.  
 XX 01-DEC-2000; 2000WO-US32703.  
 XX 03-DEC-1999; 99US-0169049.  
 XX 13-SEP-2000; 2000US-0232219.  
 XX 31-OCT-2000; 2000US-0244610.

PA (ZYMO ) ZYMOGENETICS INC.  
 XX

PI Presnell SR, Xu W, Kindsvogel W, Chen Z;  
 XX WPI; 2001-356158/37.  
 DR N-PSDB; AAF83735.  
 XX

PT New soluble cytokine receptor polypeptides and polynucleotides, useful  
 XX for diagnosing and treating cancer and inflammatory conditions -

PS Claim 1; Page 186-188; 210pp; English.  
 XX The invention relates to a human cytokine receptor polypeptide,  
 CC designated zcytor16. The zcytor16 polypeptide can be expressed by  
 CC standard recombinant methodology and can bind to IL-11F (undefined). The  
 CC zcytor16 protein is useful for: inhibiting IL-11F induced proliferation  
 CC or differentiation of hematopoietic cell(s) (progenitors); reducing  
 CC IL-11F induced or IL-9 induced inflammation; and suppressing an  
 CC inflammatory response in a mammal with inflammation; and suppressing an  
 CC multimeric receptor polypeptides such as soluble zcytor 16/CRF2-4 can be  
 CC used to reduce progression and symptoms of cancer. Zcytor16 polypeptides  
 CC can also be used to detect IL-11F levels which is indicative of  
 CC pathological conditions including inflammatory states (e.g. rheumatoid  
 CC arthritis) and cancer. Antibodies that bind zcytor16 polypeptides and the  
 CC polypeptides themselves are useful for the treatment of inflammation,  
 CC inflammatory diseases (e.g. infection, asthma, inflammatory bowel  
 CC disease, rheumatoid arthritis and atherosclerosis) and autoimmune  
 CC diseases. The antibodies and zcytor16 polynucleotides are also useful  
 CC for detecting cancer. The present sequence represents the human  
 CC zcytor16 protein.  
 XX

SQ Sequence 231 AA;  
 XX

Query Match 100.0%; Score 1244; DB 22; Length 231;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-123;  
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMEKHCFLGFLISFLLTGAVAGTSTHESLKPORVQFQSRNPNHILQMPGRALTGNSSVY 60  
 DB 1 MMEKHCFLGFLISFLLTGAVAGTSTHESLKPORVQFQSRNPNHILQMPGRALTGNSSVY 60  
 QY 61 FVQYKIYQGRQWKNEKDCWGTQELSCDLTSETSDIOEPYIGRVAAAGSYSEMSMTPRF 120  
 DB 61 FVQYKIYQGRQWKNEKDCWGTQELSCDLTSETSDIOEPYIGRVAAAGSYSEMSMTPRF 120  
 QY 121 TPWMEETKIDPPVNMNTQVNGSLVILHAHPNLPYRYQEKKNVSIEDYELLRYVFIINNSL 180  
 DB 121 TPWMEETKIDPPVNMNTQVNGSLVILHAHPNLPYRYQEKKNVSIEDYELLRYVFIINNSL 180  
 QY 181 EKEQKYVEGAHRAVEIEALTTPHSSYCVAAEIQPMLDRRSQREERCEVIEP 231  
 DB 181 EKEQKYVEGAHRAVEIEALTTPHSSYCVAAEIQPMLDRRSQREERCEVIEP 231

RESULT 4  
 AA017381

ID AA017381 standard; Protein; 231 AA.  
 XX

AC AA017381;  
 XX

DT 08-AUG-2002 (first entry)

XX Human cytokine receptor variant 2.  
 DE

XX Human; cytokine receptor; immune disease; psoriasis; cancer; infection;  
 KW rheumatoid arthritis; multiple sclerosis; Crohn's disease;  
 KW ulcerative colitis; transpant rejection; abortion; antipsoriatic;  
 KW immunosuppressive; antineumatic; antiarthritis; neuroprotective;  
 KW antineumatic; antileuk; cytosolic; dermatological;  
 KW chromosome 6q24.1-25.2; receptor.  
 XX

OS Homo sapiens.  
 XX

PN EPI191035-A2.  
 XX

XX 27-MAR-2002.  
 PD

XX 24-AUG-2001; 2001EP-0250307.  
 PF

XX 25-SEP-2000; 2000DE-1048626.  
 PR

XX 17-NOV-2000; 2000DE-1058907.  
 PR

XX 19-DEC-2000; 2000DE-1064906.  
 XX

PA (SCHD ) SCHERING AG.  
 XX

PI Weiss B, Sabat R, Assadullah K, Toshi L;  
 XX WPI; 2002-332210/37.  
 DR N-PSDB; AAL46000.  
 XX

PT New nucleic acid encoding soluble cytokine receptor, useful for  
 XX diagnosis and treatment of e.g. immune disease, also related protein  
 XX and antibodies -

PS Claim 6; Page 14; 21pp; German.  
 XX

XX The present invention provides the protein and coding sequences of 3  
 CC variants of a human cytokine receptor. The sequences can be used in the  
 CC diagnosis, prevention and treatment of immune diseases, including  
 CC psoriasis, cancer, chronic/life-threatening infections, rheumatoid  
 CC arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and  
 CC transplant rejection and in reproductive medicine, e.g. for diagnosing  
 CC abnormal immune reactions which cause abortions. The present sequence is  
 CC variant 2 of the invention.  
 XX

SQ Sequence 231 AA;  
 XX

Query Match 100.0%; Score 1244; DB 23; Length 231;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-123;  
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMEKHCFLGFLISFLLTGAVAGTSTHESLKPORVQFQSRNPNHILQMPGRALTGNSSVY 60  
 DB 1 MMEKHCFLGFLISFLLTGAVAGTSTHESLKPORVQFQSRNPNHILQMPGRALTGNSSVY 60  
 QY 61 FVQYKIYQGRQWKNEKDCWGTQELSCDLTSETSDIOEPYIGRVAAAGSYSEMSMTPRF 120  
 DB 61 FVQYKIYQGRQWKNEKDCWGTQELSCDLTSETSDIOEPYIGRVAAAGSYSEMSMTPRF 120  
 QY 121 TPWMEETKIDPPVNMNTQVNGSLVILHAHPNLPYRYQEKKNVSIEDYELLRYVFIINNSL 180  
 DB 121 TPWMEETKIDPPVNMNTQVNGSLVILHAHPNLPYRYQEKKNVSIEDYELLRYVFIINNSL 180  
 QY 181 EKEQKYVEGAHRAVEIEALTTPHSSYCVAAEIQPMLDRRSQREERCEVIEP 231  
 DB 181 EKEQKYVEGAHRAVEIEALTTPHSSYCVAAEIQPMLDRRSQREERCEVIEP 231

RESULT 5  
 AA080000

ID AA080000 standard; Protein; 231 AA.  
 XX

AC AA080000;  
 XX

Mon Jan 13 15:37:26 2003

15-JUL-2002 (first entry)

Human IL-TIF/IL-22 binding protein #1.  
Human, soluble protein; interleukin-TIF/IL-22; IL-TIF/IL-22; IL-22BP;  
IL-TIF/IL-22 antagonist.

Homo sapiens.  
WO200224912-A2.  
28-MAR-2002.

21-SEP-2001; 2001WO-US29576.  
22-SEP-2000; 2000US-234583P.  
03-NOV-2000; 2000US-245495P.  
31-JUL-2001; 2001US-0919162.

(LUDW-) LUDWIG INST CANCER RES.  
Renauld J, Dumoutier J;  
WPI: 2002-383190/41.  
N-PSDB; ABK50076.

Polynucleotide and polypeptide of soluble protein which binds to  
interleukin-TIF/IL-22 useful for inhibiting effect of IL-TIF/IL-22 on a  
cell

Claim 14; Page 39; 42pp; English.  
The present invention relates to a new polynucleotide that encodes a  
soluble protein which binds to interleukin (IL)-TIF/IL-22 (also referred  
to as IL-22BP), where the complementary sequence of the invention  
hybridises under stringent conditions to a nucleotide sequence of 2271  
or 2366 base pairs, as given in the specification. The molecules of the  
invention are useful for inhibiting (antagonising) effect of IL-TIF/IL-22  
on a cell, for determining whether IL-TIF/IL-22 is present in a sample,  
for inhibiting binding of IL-TIF/IL-22 to a binding partner, preferably  
in vitro, and for obtaining an antibody molecule specific for the soluble  
binding protein of the invention, from a population or panel of antibody  
molecules of diverse binding specificity. The soluble protein is further  
useful in manufacture of a medicament for treating an antibody or a peptide  
disease and for assaying an agent, preferably an antibody or a peptide  
fragment of IL-TIF/IL-22 or the soluble protein, that modulates binding  
of the soluble protein to IL-TIF/IL-22, where the agent identified is  
used in the manufacture of medicament for treating IL-TIF/IL-22 mediated  
disorder. The antibody is useful for determining presence of the soluble  
protein, where the antibody is detectably labelled. The present amino  
acid sequence represents the human IL-TIF/IL-22 binding protein #1 of  
the invention.

Query Match 100.0%; Score 1244; DB 23; Length 231;  
Best Local Similarity 100.0%; Pred. No. 1.1e-123; Indels 0; Gaps 0;  
Matches 231; Conservative 0; Mismatches 0;

1 MWPKHCFGLISFLFTGVAGTQSTHSLKPVQVQSRNFHNLQWQGRALTGNSVY 60  
1 MWPKHCFGLISFLFTGVAGTQSTHSLKPVQVQSRNFHNLQWQGRALTGNSVY 60

61 FVQYKIYQORQWKNECDWGTQSLTSETSDIQEPIYGRVRAASAGSYSEWSTPFR 120  
61 FVQYKIYQORQWKNECDWGTQSLTSETSDIQEPIYGRVRAASAGSYSEWSTPFR 120

121 TPWETKIDPPVNMITQVNGSLLVILHAPNLPRYQKEKNVSDIYELLYRVFIINNSL 180  
121 TPWETKIDPPVNMITQVNGSLLVILHAPNLPRYQKEKNVSDIYELLYRVFIINNSL 180

181 EKEQKYEGAHRAVEIEALTPHSSYCVVAEIQPMLDRRSQSRSERCVEIP 231  
181 EKEQKYEGAHRAVEIEALTPHSSYCVVAEIQPMLDRRSQSRSERCVEIP 231

181 EKEQKYEGAHRAVEIEALTPHSSYCVVAEIQPMLDRRSQSRSERCVEIP 231

RESULT 6  
ABG34086  
ID ABG34086 standard; Protein; 231 AA.

XX AC ABG34086;  
XX 15-JUL-2002 (first entry)

XX Human Pro peptide #57.  
XX Human; PRO; secreted protein; transmembrane protein;  
XX genetic disorder; tumour; cancer.

XX Homo sapiens.  
XX WO200224888-A2.  
XX 28-MAR-2002.

XX 29-AUG-2001; 2001WO-US27099.  
XX 01-SEP-2000; 2000US-229896P.  
XX 05-SEP-2000; 2000US-230621P.  
XX 12-SEP-2000; 2000US-235147P.  
XX 10-NOV-2000; 2000WO-US30873.  
XX 12-JAN-2001; 2001US-261878P.  
XX 16-JAN-2001; 2001US-261910P.  
XX 16-JAN-2001; 2001US-261939P.  
XX 16-JAN-2001; 2001US-262150P.  
XX 25-JAN-2001; 2001US-264395P.  
XX 02-FEB-2001; 2001US-266421P.  
XX 09-FEB-2001; 2001US-267623P.  
XX 28-FEB-2001; 2001WO-US06520.  
XX 09-MAR-2001; 2001US-274399P.  
XX 03-APR-2001; 2001US-280982P.  
XX 04-APR-2001; 2001US-282129P.  
XX 04-APR-2001; 2001US-282199P.  
XX 09-MAY-2001; 2001US-290589P.  
XX 25-MAY-2001; 2001WO-US17092.  
XX 01-JUN-2001; 2001WO-US17800.  
XX 20-JUN-2001; 2001WO-US19692.  
XX 29-JUN-2001; 2001WO-US21066.  
XX 09-JUL-2001; 2001WO-US21735.

(GETH ) GENENTECH INC.  
Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,  
Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;  
Fong S;  
WPI: 2002-362426/39.  
N-PSDB; ABK70017.

New PRO polypeptides and polynucleotides encoding the polypeptides,  
useful in gene therapy, chromosome identification, tissue typing, or  
for genetic analysis of individuals with genetic disorders

Claim 11; Figure 114; 218pp; English.  
This invention relates to the cDNA and protein sequences of novel  
secreted and transmembrane polypeptides PRO polypeptides. The  
invention also comprises a method for producing the proteins of the  
invention by recombinant means and antibodies specific for the protein  
of the invention. The antibody may be used for detecting the PRO  
proteins of the invention and may be used to modify their activity.  
Polynucleotides may be used as hybridisation probes for a cDNA library  
to isolate the full-length PRO cDNA or to isolate other cDNAs, to  
construct hybridisation probes for mapping the gene which encodes that  
PRO and for genetic analysis of individuals with genetic disorders, in  
assays to identify other proteins or molecules involved in binding

CC reaction, to generate transgenic animals or knock-out animals which in  
CC turn are useful in the development and screening of therapeutically  
CC useful reagents, for chromosome identification, and tissue typing. The  
CC PRO polypeptides are useful in gene therapy, and as molecular weight  
CC markers for protein electrophoresis purposes. The sequences may  
CC also be used to detect overexpression on PRO polypeptides in cancerous  
CC tumours and for screening for differentially expressed genes using  
CC microarray technology. The present sequence represents a human PRO  
CC protein of the invention.

XX Sequence 231 AA;

Query Match 100.0%; Score 1244; DB 23; Length 231;  
Best Local Similarity 100.0%; Pred. No. 1,1e-123;  
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPPKHCFLGLISFPLTGVAGTSTHESLKPORVQFSRNFNIIOMOPGRALTGNSSVY 60  
DB 1 MPPKHCFLGLISFPLTGVAGTSTHESLKPORVQFSRNFNIIOMOPGRALTGNSSVY 60  
QY 61 FVOYKTYGQROMKKNKEDCWTGELSCDLTSETSDIOEPYGRVRAASAGSYSEWMTPRF 120  
DB 61 FVOYKTYGQROMKKNKEDCWTGELSCDLTSETSDIOEPYGRVRAASAGSYSEWMTPRF 120  
QY 121 TPWWEKIDPPVNNITOVNGSLVILHAPNLPYRQKKNVSIIDYVELLRVFIINNSL 180  
DB 121 TPWWEKIDPPVNNITOVNGSLVILHAPNLPYRQKKNVSIIDYVELLRVFIINNSL 180  
QY 181 EKEQKYEGAHRAVEIEALTPHSSYCVVAEITYOPMLDRSQRSERCVEIP 231  
DB 181 EKEQKYEGAHRAVEIEALTPHSSYCVVAEITYOPMLDRSQRSERCVEIP 231

RESULT 7

ID AAE17320 standard; Protein; 231 AA.

XX AAE17320;

DT 18-APR-2002 (first entry)

DE Human cytokine receptor protein, sbg456548CytocRa #2.

XX Human; therapy; wound healing disorder; vaccine; cancer; infection;  
KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;  
KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;  
KW multiple sclerosis; Alzheimer's disease; analgesic; cardiac; asthma;  
KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;  
KW depression; cardiovascular disease; myocardial infarction; renal failure;  
KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;  
KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;  
KW hyperplasia; renal disease; hypoglycaemia; gastrointestinal disease;  
KW nocturnal; cirrhosis; Hodgkin's disease; neuroleptic; anti-inflammatory;  
KW haemoblastic; vulvar; anticonvulsant; antineoplastic; neuroprotective;  
KW nephrotropic; hypotensive; vasotropic; cytosolic; cerebroprotective;  
KW allergy; cytokine receptor.

OS Homo sapiens.

XX WO200198342-A1.

XX 27-DEC-2001.

XX 22-JUN-2001; 2001WO-US19929.

XX 22-JUN-2000; 2000US-213156P.

XX 22-JUN-2000; 2000US-213161P.

XX (SMK) SMITHKLINE BEECHAM CORP.

XX (SMK) SMITHKLINE BEECHAM PLC.

XX (GLAX) GLAXO GROUP LTD.

PI Agarwal P, Cogswell JP, Kabnlic KS, Lai Y, Martensen SA;

PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;  
XX WPI: 2002-139783/18.  
DR N-PSDB; AAD27815.

PT Novel secreted and membrane-associated polypeptides and polynucleotides  
PT useful for preventing, ameliorating or correcting dysfunction or  
PT abnormalities -  
PS Claim 1; Page 132-133; 138pp; English.

XX The invention relates to secreted and membrane-associated polypeptides  
CC and polynucleotides. The sequences of the invention are useful in  
CC diagnostic assays for detecting diseases associated with inappropriate  
CC activity or levels of these polynucleotides, and in identifying their  
CC agonists and antagonists that are potentially useful in therapy. The  
CC sequences of the invention are useful as vaccines for inducing  
CC immunological response. The sequences of the invention are useful for  
CC treating cancers, infections, autoimmune disorders, haematopoietic  
CC disorders, wound healing disorders, cholesterol disorders, storage disease,  
CC inflammation, congenital muscular dystrophy, junctional epidermolysis  
CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,  
CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,  
CC septicemia, psoriasis, inflammatory bowel disease, transplant rejection,  
CC graft versus host disease, ischaemia, stroke, acute respiratory disease  
CC syndrome, restenosis, brain injury, AIDS, bone disease, atherosclerosis,  
CC brain disorders including paraneoplastic palsy, myotonic dystrophy,  
CC depression, anxiety disorders and sleep disorders, cardiovascular  
CC diseases including congestive heart failure and myocardial infarction,  
CC respiratory diseases including chronic obstructive pulmonary disease,  
CC including bronchitis and adult respiratory distress syndrome, liver disorders  
CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral  
CC and non-viral hepatitis, type II diabetes mellitus, renal disease  
CC including acute and chronic renal failure, glomerulonephritis, Fanconi's  
CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia  
CC and tendinitis, gastrointestinal diseases including intestinal  
CC obstruction and tropical sprue, spleen disorders including hypersplenism,  
CC Hodgkin's disease and malignant lymphoma, testicular cancer, male  
CC reproductive diseases including low testosterone and male infertility.  
CC The present sequence is human cytokine receptor.

XX Sequence 231 AA;

Query Match 100.0%; Score 1244; DB 23; Length 231;  
Best Local Similarity 100.0%; Pred. No. 1,1e-123;  
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPPKHCFLGLISFPLTGVAGTSTHESLKPORVQFSRNFNIIOMOPGRALTGNSSVY 60  
DB 1 MPPKHCFLGLISFPLTGVAGTSTHESLKPORVQFSRNFNIIOMOPGRALTGNSSVY 60  
QY 61 FVOYKTYGQROMKKNKEDCWTGELSCDLTSETSDIOEPYGRVRAASAGSYSEWMTPRF 120  
DB 61 FVOYKTYGQROMKKNKEDCWTGELSCDLTSETSDIOEPYGRVRAASAGSYSEWMTPRF 120  
QY 121 TPWWEKIDPPVNNITOVNGSLVILHAPNLPYRQKKNVSIIDYVELLRVFIINNSL 180  
DB 121 TPWWEKIDPPVNNITOVNGSLVILHAPNLPYRQKKNVSIIDYVELLRVFIINNSL 180  
QY 181 EKEQKYEGAHRAVEIEALTPHSSYCVVAEITYOPMLDRSQRSERCVEIP 231  
DB 181 EKEQKYEGAHRAVEIEALTPHSSYCVVAEITYOPMLDRSQRSERCVEIP 231

RESULT 8

ID AAU80324 standard; Protein; 263 AA.

XX AAU80324;

DT 15-JUL-2002 (first entry)



XX DE Human IL-TIF/IL-22 binding protein #2.  
 XX KW Human; soluble protein; interleukin-TIF/IL-22; IL-TIF/IL-22; IL-22BP;  
 KW KW IL-TIF/IL-22 antagonist.  
 XX OS Homo sapiens.  
 XX XX WO200224912-A2.  
 XX PD 28-MAR-2002.  
 XX PF 21-SEP-2001; 2001WO-US29576.  
 XX PR 22-SEP-2000; 2000US-234583P.  
 XX PR 03-NOV-2000; 2000US-245495P.  
 XX PR 31-JUL-2001; 2001US-091916Z.  
 XX PA (LUDW-) LUDWIG INST CANCER RES.  
 XX PI Renaud J, Dumoutier L;  
 XX XX WPI; 2002-383190/41.  
 XX DR N-PSDB; ABK50080.  
 XX XX Polynucleotide and polypeptide of soluble protein which binds to  
 PT interleukin-TIF/IL-22 useful for inhibiting effect of IL-TIF/IL-22 on a  
 PT cell -  
 XX XX Claim 14; Page 41-42; 42pp; English.  
 XX CC The present invention relates to a new polynucleotide that encodes a  
 CC soluble protein which binds to interleukin (IL)-TIF/IL-22 (also referred  
 CC to as IL-22BP), where the complementary sequence of the invention  
 CC hybridises under stringent conditions to a nucleotide sequence of 2271  
 CC or 2366 base pairs, as given in the specification. The molecules of the  
 CC invention are useful for inhibiting (antagonising) effect of IL-TIF/IL-22  
 CC on a cell, for determining whether IL-TIF/IL-22 is present in a sample,  
 CC for inhibiting binding of IL-TIF/IL-22 to a binding partner, preferably  
 CC in vitro, and for obtaining an antibody molecule specific for the soluble  
 CC binding protein of the invention, from a population or panel of antibody  
 CC molecules of diverse binding specificity. The soluble protein is further  
 CC useful in manufacture of a medicament for treating an IL-22 mediated  
 CC disease and for assaying an agent, preferably an antibody or a peptide  
 CC fragment of IL-TIF/IL-22 or the soluble protein, that modulates binding  
 CC of the soluble protein to IL-TIF/IL-22, where the agent identified is  
 CC used in the manufacture of medicament for treating IL-TIF/IL-22 mediated  
 CC disorder. The antibody is useful for determining presence of the soluble  
 CC protein, where the antibody is detectably labelled. The present amino  
 CC acid sequence represents the human IL-TIF/IL-22 binding protein #2 of  
 CC the invention.  
 XX SQ Sequence 263 AA;  
 Query Match 97.9%; Score 1218; DB 23; Length 263;  
 Best Local Similarity 87.8%; Pred. No. 7.5e-121;  
 Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;  
 QY 1 MPMKPCFLGLISFETGVAGTOSTHESLKQVQVQSRNFHNLQWQGRALTGNSVY 60  
 DB 1 MPMKPCFLGLISFETGVAGTOSTHESLKQVQVQSRNFHNLQWQGRALTGNSVY 60  
 QY 61 FVOYKI-----YGRQWKNEKDCWGTQELSCDL 88  
 DB 61 FVOYKIMFSCMSKSSHQSDVAMQHSICNPPGCGTCLAKYQGRQWKNEKDCWGTQELSCDL 120  
 QY 89 TSETSDIQEYGRVRAASAGSYSEWSMTFRFPWETKIDPPVNMITQVNSLLVILHA 148  
 DB 121 TSETSDIQEYGRVRAASAGSYSEWSMTFRFPWETKIDPPVNMITQVNSLLVILHA 180  
 QY 149 PNLPRYQKEKNYSIEDYELLXRVFTIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV 208  
 DB 181 PNLPRYQKEKNYSIEDYELLXRVFTIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV 240

QY 209 AEIYQPMLEDRSRQSEERCVEIP 231  
 DB 241 AEIYQPMLEDRSRQSEERCVEIP 263  
 RESULT 9  
 AAE17321  
 ID AAE17321 standard; Protein; 263 AA.  
 XX AAE17321;  
 AC AAE17321;  
 DT 18-APR-2002 (first entry)  
 XX Human cytokine receptor protein, sbg45548CytRa #3.  
 DE Human; therapy; wound healing disorder; vaccine; cancer; infection;  
 XX autoimmune disorder; haematopoietic disorder; inflammation; arthritis;  
 KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;  
 KW multiple sclerosis; Alzheimer's disease; analgesic; cardiac; asthma;  
 KW ischaemia; stroke; bone disease; atherosclerosis; brain disorder;  
 KW depression; cardiovascular disease; myocardial infarction; renal failure;  
 KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;  
 KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;  
 KW hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;  
 KW neutropenic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;  
 KW haemostatic; vulnery; anticonvulsant; antirheumatic; neuroprotective;  
 KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;  
 KW allergy; cytokine receptor.  
 XX Homo sapiens.  
 OS WO200198342-A1.  
 XX 27-DEC-2001.  
 XX 22-JUN-2001; 2001WO-US19929.  
 XX 22-JUN-2000; 2000US-213156P.  
 XX 22-JUN-2000; 2000US-213161P.  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX (GLAX ) GLAXO GROUP LTD.  
 XX Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;  
 PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;  
 XX WPI; 2002-139783/18.  
 XX N-PSDB; AAD27816.  
 XX Novel secreted and membrane-associated polypeptides and polynucleotides  
 PT useful for preventing, ameliorating or correcting dysfunction or  
 PT disease including diabetes, cancer, hypertension and growth  
 PT abnormalities -  
 XX Claim 1; Page 133-134; 138pp; English.  
 XX The invention relates to secreted and membrane-associated polypeptides  
 CC and polynucleotides. The sequences of the invention are useful in  
 CC diagnostic assays for detecting diseases associated with inappropriate  
 CC activity or levels of these polynucleotides, and in identifying their  
 CC agonists and antagonists that are potentially useful in therapy. The  
 CC sequences of the invention are useful as vaccines for inducing  
 CC immunological response. The sequences of the invention are useful for  
 CC treating cancers, infections, autoimmune disorders, haematopoietic  
 CC disorders, wound healing disorders, cholesterol ester storage disease,  
 CC inflammation, congenital muscular dystrophy, junctional epidermolysis  
 CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,  
 CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,  
 CC allergies, schizophrenia, sbg44244SPROA-associated disorders,  
 CC septicemia, psoriasis, inflammatory bowel disease, transplant rejection,  
 CC graft versus host disease, ischaemia, stroke, acute respiratory disease



CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,  
 CC brain disorders including paraaortic/paracardiac palsy, myotonic dystrophy,  
 CC depression, anxiety disorders and sleep disorders, cardiovascular  
 CC diseases including congestive heart failure and myocardial infarction,  
 CC respiratory diseases including chronic obstructive pulmonary disease,  
 CC acute bronchitis and adult respiratory distress syndrome, liver disorders  
 CC including hypercholesterolemia, hypertriglyceridemia, cirrhosis, viral  
 CC and non-viral hepatitis, type II diabetes mellitus, renal disease  
 CC including acute and chronic renal failure, glomerulonephritis, Fanconi's  
 CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia  
 CC and tendinitis, gastrointestinal diseases including intestinal  
 CC obstruction and tropical sprue, spleen disorders including hyperplasia  
 CC Hodgkin's disease and malignant lymphoma, testicular cancer, male  
 CC reproductive diseases including low testosterone and male infertility.  
 CC The present sequence is human cytokine receptor.

XX Sequence 263 AA;

Query Match

Best Local Similarity 97.9%; Score 1219; DB 23; Length 263;  
 Chs 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MPMKICFLGFLISFLTVAGTOSTHESLKPQVQFOSRNFHNILOMOPGRALTGNSSVY 60  
 DB 1 MPMKICFLGFLISFLTVAGTOSTHESLKPQVQFOSRNFHNILOMOPGRALTGNSSVY 60  
 QY 61 FVOYKI-----YGORQKXKEDCKGTOELSCDL 88  
 DB 61 FVOYKIMFSCSMKSHQKPGSCQWHSICNPGCRTLAKYGQKQKXKEDCKGTOELSCDL 120  
 QY 89 TSETSDIOEPPYGRVRAASAGSYSEMSWTPRFTPMWETKIDPPVNNITQVNGSLVILHA 148  
 DB 121 TSETSDIOEPPYGRVRAASAGSYSEMSWTPRFTPMWETKIDPPVNNITQVNGSLVILHA 180  
 QY 149 PNLPRYQKKNVSIEDYELLRVFIIINNSLEKEQKVEGAHRAVEIEALTPHSSYCV 208  
 DB 181 PNLPRYQKKNVSIEDYELLRVFIIINNSLEKEQKVEGAHRAVEIEALTPHSSYCV 240  
 QY 209 AEIYQPMIDRRSRQSERCEIP 231  
 DB 241 AEIYQPMIDRRSRQSERCEIP 263

RESULT 10

ID AA017382 standard; Protein: 263 AA.

XX AC AA017382;

XX 08-AUG-2002 (first entry)

XX Human cytokine receptor variant 3.

XX Human; cytokine receptor; immune disease; psoriasis; cancer; infection;  
 KW rheumatoid arthritis; multiple sclerosis; Crohn's disease;  
 KW ulcerative colitis; transplant rejection; abortion; antipsoriatic;  
 KW immunosuppressive; antineoplastic; antidiabetic; neuroprotective;  
 KW antiinflammatory; antitumor; cytostatic; dermatological;  
 KW chromosome 6q24.1-25.2; receptor.

XX Homo sapiens.

XX EP191035-A2.

XX 27-MAR-2002.

XX 24-AUG-2001; 2001EP-0250307.

XX 25-SEP-2000; 2000DE-1048626.

XX 17-NOV-2000; 2000DE-1058907.

XX 19-DEC-2000; 2000DE-1064906.

XX (SCHD) SCHERING AG.

XX Weis B, Sabat R, Assadullah K, Toshi L;  
 PI WPT: 2002-332210/37.  
 DR N-PSDB; AAL46001.  
 XX New nucleic acid encoding soluble cytokine receptor, useful for  
 PT diagnosis and treatment of e.g. immune disease, also related protein  
 PT and antibodies  
 PS Claim 6; Page 15; 21pp; German.  
 XX The present invention provides the protein and coding sequences of 3  
 CC variants of a human cytokine receptor. The sequences can be used in the  
 CC diagnosis, prevention and treatment of immune diseases, including  
 CC psoriasis, cancer, chronic/life-threatening infections, rheumatoid  
 CC arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and  
 CC transplant rejection and in reproductive medicine, e.g. for diagnosing  
 CC abnormal immune reactions which cause abortions. The present sequence is  
 CC variant 3 of the invention.

XX Sequence 263 AA;

Query Match

Best Local Similarity 97.6%; Score 1214; DB 23; Length 263;  
 Matches 230; Conservative 1; Mismatches 0; Indels 32; Gaps 1;

QY 1 MPMKICFLGFLISFLTVAGTOSTHESLKPQVQFOSRNFHNILOMOPGRALTGNSSVY 60  
 DB 1 MPMKICFLGFLISFLTVAGTOSTHESLKPQVQFOSRNFHNILOMOPGRALTGNSSVY 60  
 QY 61 FVOYKI-----YGORQKXKEDCKGTOELSCDL 88  
 DB 61 FVOYKIMFSCSMKSHQKPGSCQWHSICNPGCRTLAKYGQKQKXKEDCKGTOELSCDL 120  
 QY 89 TSETSDIOEPPYGRVRAASAGSYSEMSWTPRFTPMWETKIDPPVNNITQVNGSLVILHA 148  
 DB 121 TSETSDIOEPPYGRVRAASAGSYSEMSWTPRFTPMWETKIDPPVNNITQVNGSLVILHA 180  
 QY 149 PNLPRYQKKNVSIEDYELLRVFIIINNSLEKEQKVEGAHRAVEIEALTPHSSYCV 208  
 DB 181 PNLPRYQKKNVSIEDYELLRVFIIINNSLEKEQKVEGAHRAVEIEALTPHSSYCV 240  
 QY 209 AEIYQPMIDRRSRQSERCEIP 231  
 DB 241 AEIYQPMIDRRSRQSERCEIP 263

RESULT 11

ID AAU09186 standard; Protein: 262 AA.

XX AAU09186;

XX 16-JUN-2002 (first entry)

XX Human PRO19598 polypeptide.

XX Human; PRO19598; clone DNA145887; immune-related disorder;  
 KW inflammatory disorder; infectious disorder; immunodeficiency disorder;  
 KW autoimmune disorder; renal disease; demyelinating disease; skin disease;  
 KW neoplasia; transplantation associated disease; immunosuppressive;  
 KW anti-inflammatory; antisthmatic; antidiabetic.

XX Homo sapiens.

XX Key

XX Peptide 1..20 Location/Qualifiers

XX Modified-site 17..22 /label= Signal\_peptide

XX Modified-site 20..25 /note= "N-myristoylation site"

XX /note= "N-myristoylation site"

Protein 21..262  
 /label= Mature\_PRO19598\_polypeptide  
 Modified-site 55..58  
 /note= "N-glycosylation site"  
 Modified-site 165..168  
 /note= "N-glycosylation site"  
 Modified-site 170..173  
 /note= "N-glycosylation site"  
 Modified-site 191..194  
 /note= "N-glycosylation site"  
 Modified-site 208..211  
 /note= "N-glycosylation site"  
 Modified-site 220..225  
 /note= "N-myristoylation site"

WO200166740-A2.

13-SEP-2001.

01-MAR-2001; 2001WO-US06666.

03-MAR-2000; 2000US-187202P.

21-MAR-2000; 2000US-191015P.

30-MAY-2000; 2000WO-US14941.

05-JUN-2000; 2000US-209832P.

24-AUG-2000; 2000WO-US23328.

01-DEC-2000; 2000WO-US26678.

(GETH ) GENENTECH INC.

Eaton DL, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;  
 Tumas D, Watanabe CK, Wood WL, Zhang Z;

WPI; 2001-625876/72.

N-P5DB; AAS15368.

Nucleic acids encoding PRO polypeptides, useful for detecting and  
 treating immune related diseases and disorders in mammals including  
 autoimmune diseases, inflammatory diseases and asthma

Claim 10; Fig 18; 122pp; English.

The present invention relates to the isolation of 9 novel human PRO  
 polypeptides and the cDNA sequences (AAS15360-AAS15368) encoding them.  
 The novel PRO polypeptides include PRO1356, PRO1268, PRO1884, PRO3444,  
 PRO3151, PRO4322, PRO9964, PRO10008 and PRO19598. The cDNA sequences  
 encoding these PRO polypeptides have been designated as clones  
 DNA64886-1601, DNA64903-1553, DNA84318-2520, DNA87997, DNA89273,  
 DNA92223-2567, DNA96973, DNA101921 and DNA145887 respectively.  
 Compositions (e.g. vaccines) containing PRO polypeptides and methods of  
 using these compositions are useful in the treatment and diagnosis of  
 immune-related disorders. Such disorders include immune-mediated  
 inflammatory disorders (e.g. osteoarthritis), non-immune-mediated  
 inflammatory disorders (e.g. diabetes mellitus), infectious disorders  
 (e.g. granulomatous hepatitis), immunodeficiency disorders (e.g. AIDS),  
 autoimmune disorders (e.g. rheumatoid arthritis), immune-related renal  
 diseases (e.g. cirrhosis), demyelinating diseases of the peripheral or  
 central nervous system (e.g. Guillain-Barre syndrome), immune-mediated  
 skin diseases (e.g. contact dermatitis), neoplasias and transplantation  
 associated diseases. The polynucleotide sequences of the invention may  
 be used in gene therapy. AAU09178-AAU09186 represent the novel human  
 PRO polypeptides of the invention.

Sequence 262 AA;

Query Match 97.5%; Score 1213; DB 22; Length 262;

Best Local Similarity 87.8%; Pred. No. 2.5e-120;

Matches 230; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 2 MPKRCFLGLISFLTGAGTQSTHSLKPKQVQFQSRNFHNLQWPGRLTGNSVYF 61

Db 1 MPKRCFLGLISFLTGAGTQSTHSLKPKQVQFQSRNFHNLQWPGRLTGNSVYF 60

QY 62 VOYKI-----YQORWKNKEDCWGCTOELSCDLT 89  
 Db 61 VOYKIMFSCMKSSHQSPGQWQHISCNFPQCRTLAKYQORWKNKEDCWGCTOELSCDLT 120  
 QY 90 SETSDIQBPYGRVRAAGSAGSYSEWSMTPTPTWWTETKIDPPVNMNITQVNGSLLVILHAP 149  
 Db 121 SETSDIQBPYGRVRAAGSAGSYSEWSMTPTPTWWTETKIDPPVNMNITQVNGSLLVILHAP 180  
 QY 150 NLPYRYQKEKNVSIEDYVELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 209  
 Db 181 NLPYRYQKEKNVSIEDYVELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVA 240  
 QY 210 EYQPMLEDRRSORSERCEVEIP 231  
 Db 241 EYQPMLEDRRSORSERCEVEIP 262

RESULT 12  
 AAE17319  
 ID AAE17319 standard; Protein; 214 AA.  
 XX  
 AC AAE17319;  
 XX  
 DT 18-APR-2002 (first entry)  
 XX  
 DE Human cytokine receptor protein, sbg456548CytoRa #1.  
 XX  
 KW Human; therapy: wound healing disorder; vaccine; cancer; infection;  
 KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;  
 KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;  
 KW multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;  
 KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;  
 KW depression; cardiovascular disease; myocardial infarction; renal failure;  
 KW respiratory disease; liver disorder; skeletal muscle disorder; immunosuppressive;  
 KW type II diabetes mellitus; type I diabetes mellitus; gastrointestinal disease;  
 KW hyperplasia; renal disease; hypoglycaemia; neuroleptic; antiinflammatory;  
 KW neoplastic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;  
 KW haemostatic; vulnary; anticonvulsant; antirheumatic; neuroprotective;  
 KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;  
 KW allergy; cytokine receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200198342-A1.  
 XX  
 PD 27-DEC-2001.  
 XX  
 PF 22-JUN-2001; 2001WO-US19929.  
 XX  
 PR 22-JUN-2000; 2000US-213156P.  
 XX  
 PR 22-JUN-2000; 2000US-213161P.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA (GLAX ) GLAXO GROUP LTD.  
 XX  
 PI Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;  
 PI Murdoch PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;  
 XX  
 DR WPI; 2002-139783/18.  
 XX  
 DR N-P5DB; AAD27814.  
 XX  
 PT Novel secreted and membrane-associated polypeptides and polynucleotides  
 PT useful for preventing, ameliorating or correcting dysfunction or  
 PT disease including diabetes, cancer, hypertension and growth  
 PT abnormalities  
 XX  
 PS Claim 1; Page 122; 138pp; English.  
 XX  
 CC The invention relates to secreted and membrane-associated polypeptides  
 CC and polynucleotides. The sequences of the invention are useful in  
 CC diagnostic assays for detecting diseases associated with inappropriate  
 CC activity or levels of these polynucleotides, and in identifying their

CC agonists and antagonists that are potentially useful in therapy. The  
 CC immunological response. The sequences of the invention are useful for inducing  
 CC treating cancers, infections, autoimmune disorders, haematopoietic  
 CC disorders, wound healing disorders, cholesteryl ester storage disease,  
 CC inflammation, congenital muscular dystrophy, junctional epidermolysis  
 CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,  
 CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,  
 CC allergies, schizophrenia, Sbg442445PPOA-associated disorder,  
 CC septicemia, psoriasis, inflammatory bowel disease, transplant rejection,  
 CC graft versus host disease, ischemia, stroke, acute respiratory disease  
 CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,  
 CC brain disorders including paraparesis, palsy, myotonic dystrophy,  
 CC depression, anxiety disorders and sleep disorders, cardiovascular  
 CC diseases including congestive heart failure and myocardial infarction,  
 CC respiratory diseases including chronic obstructive pulmonary disease,  
 CC acute bronchitis and adult respiratory distress syndrome, liver disorders  
 CC including hypercholesterolemia, hypertriglyceridemia, cirrhosis, viral  
 CC and non-viral hepatitis, type II diabetes mellitus, renal disease  
 CC including acute and chronic renal failure, glomerulonephritis, Fanconi's  
 CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia  
 CC and tendinitis, gastrointestinal diseases including intestinal  
 CC obstruction and tropical sprue, spleen disorders including hypersplenism,  
 CC Hodgkin's disease and malignant lymphoma, testicular cancer, male  
 CC reproductive diseases including low testosterone and male infertility.  
 CC The present sequence is human cytokine receptor.

CC Sequence 214 AA:

Query Match 91.6%; Score 1140; DB 23; Length 214;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-112;  
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 AGTSTHSLKRPQVQFSRNFHNLQWQGRALTGNSVYFQYKTYGQRQKNKEDCW 79  
 DB 3 AGTOS--HESLXQVQFQFSRNFHNLQWQGRALTGNSVYFQYKTYGQRQKNKEDCW 62  
 QY 80 GTQELSCDLTSETSDIOEPYGRVRAASAGSYSEMSMTPTPTPWEKIDPPVNNITQVNGS 139  
 DB 63 GTQELSCDLTSETSDIOEPYGRVRAASAGSYSEMSMTPTPTPWEKIDPPVNNITQVNGS 122  
 QY 140 GSLVLIHAPNLPRYQKEKNSIEDYELLRYVFIINNSLEKQKYEGAHAVEIEALTTP 199  
 DB 123 GSLVLIHAPNLPRYQKEKNSIEDYELLRYVFIINNSLEKQKYEGAHAVEIEALTTP 182  
 QY 200 TPSSYCVVAETIYQPMIDRSQRSEERCVEIP 231  
 DB 183 TPSSYCVVAETIYQPMIDRSQRSEERCVEIP 214

RESULT 13

ID AAB62663 standard; Protein; 210 AA.

AC AAB62663;

DT 23-JUL-2001 (first entry)

DE Human zcytor16 extracellular domain fragment (residues 22-231).

KM Cytokine receptor; zcytor16; IL-TIF; antiinflammatory; cytostatic;  
 KM antithematic; antiarthritic; antiaschematic; antiatherosclerotic;  
 KM immunosuppressive; chromosome 6q24.1-25.2; human.

OS Homo sapiens.

PN MO200140467-A1.

PD 07-JUN-2001.

PF 01-DEC-2000; 2000MO-US32703.

PR 03-DEC-1999; 99US-0169049.

PR 13-SEP-2000; 2000US-0232219.  
 PR 31-OCT-2000; 2000US-0244610.  
 XX (ZYMO ) ZYMOGENETICS INC.  
 XX  
 XX Presnell SR, Xu W, Kindsvogel W, Chen Z,  
 XX WPI; 2001-356158/37.

PT New soluble cytokine receptor polypeptides and polynucleotides, useful  
 for diagnosing and treating cancer and inflammatory conditions -  
 PS Claim 1; Page 193; 210pp; English.

CC The invention relates to a human cytokine receptor polypeptide,  
 CC designated zcytor16. The zcytor16 polypeptide can be expressed by  
 CC standard recombinant methodology and can bind to IL-TIF (undefined). The  
 CC zcytor16 protein is useful for: inhibiting IL-TIF induced proliferation  
 CC or differentiation of hematopoietic cells (s) (progenitors); reducing  
 CC IL-TIF induced or IL-9 induced inflammation; and suppressing an  
 CC inflammatory response in a mammal with inflammation. Heteromeric/  
 CC multimeric receptor polypeptides such as soluble zcytor 16/CRP2-4 can be  
 CC used to reduce progression and symptoms of cancer. Zcytor16 polypeptides  
 CC can also be used to detect IL-TIF levels which is indicative of  
 CC pathological conditions including inflammatory states (e.g. rheumatoid  
 CC arthritis) and cancer. Antibodies that bind zcytor16 polypeptides and the  
 CC inflammatory diseases (e.g. infection, asthma, inflammatory bowel  
 CC disease, rheumatoid arthritis and atherosclerosis) and autoimmune  
 CC diseases. The antibodies and zcytor16 polynucleotides are also useful  
 CC for detecting cancer. The present sequence represents the human zcytor16  
 CC extracellular domain fragment.

CC Sequence 210 AA:

Query Match 90.8%; Score 1130; DB 22; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 1,2e-111;  
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TOSTHSLKRPQVQFSRNFHNLQWQGRALTGNSVYFQYKTYGQRQKNKEDCWGT 81  
 DB 1 TOSTHSLKRPQVQFSRNFHNLQWQGRALTGNSVYFQYKTYGQRQKNKEDCWGT 60  
 QY 82 QELSCDLTSETSDIOEPYGRVRAASAGSYSEMSMTPTPTPWEKIDPPVNNITQVNGS 141  
 DB 61 QELSCDLTSETSDIOEPYGRVRAASAGSYSEMSMTPTPTPWEKIDPPVNNITQVNGS 120  
 QY 142 LVITLHAPNLPRYQKEKNSIEDYELLRYVFIINNSLEKQKYEGAHAVEIEALTTP 201  
 DB 121 LVITLHAPNLPRYQKEKNSIEDYELLRYVFIINNSLEKQKYEGAHAVEIEALTTP 180  
 QY 202 HSSYCVVAETIYQPMIDRSQRSEERCVEIP 231  
 DB 181 HSSYCVVAETIYQPMIDRSQRSEERCVEIP 210

RESULT 14

ID AAE02458

AC AAE02458 standard; Protein; 249 AA.

AC AAE02458;

DT 10-AUG-2001 (first entry)

DE Human DNAX cytokine receptor subunit 4.1 (DCRS4.1).

KM Human; immunomodulator; DNAX cytokine receptor subunit 4.1; DCRS4.1;  
 KM therapy; immunological disorder; drug screening; cell development;  
 KM chromosome 6q24.1-25.2.

OS Homo sapiens.

XX Key

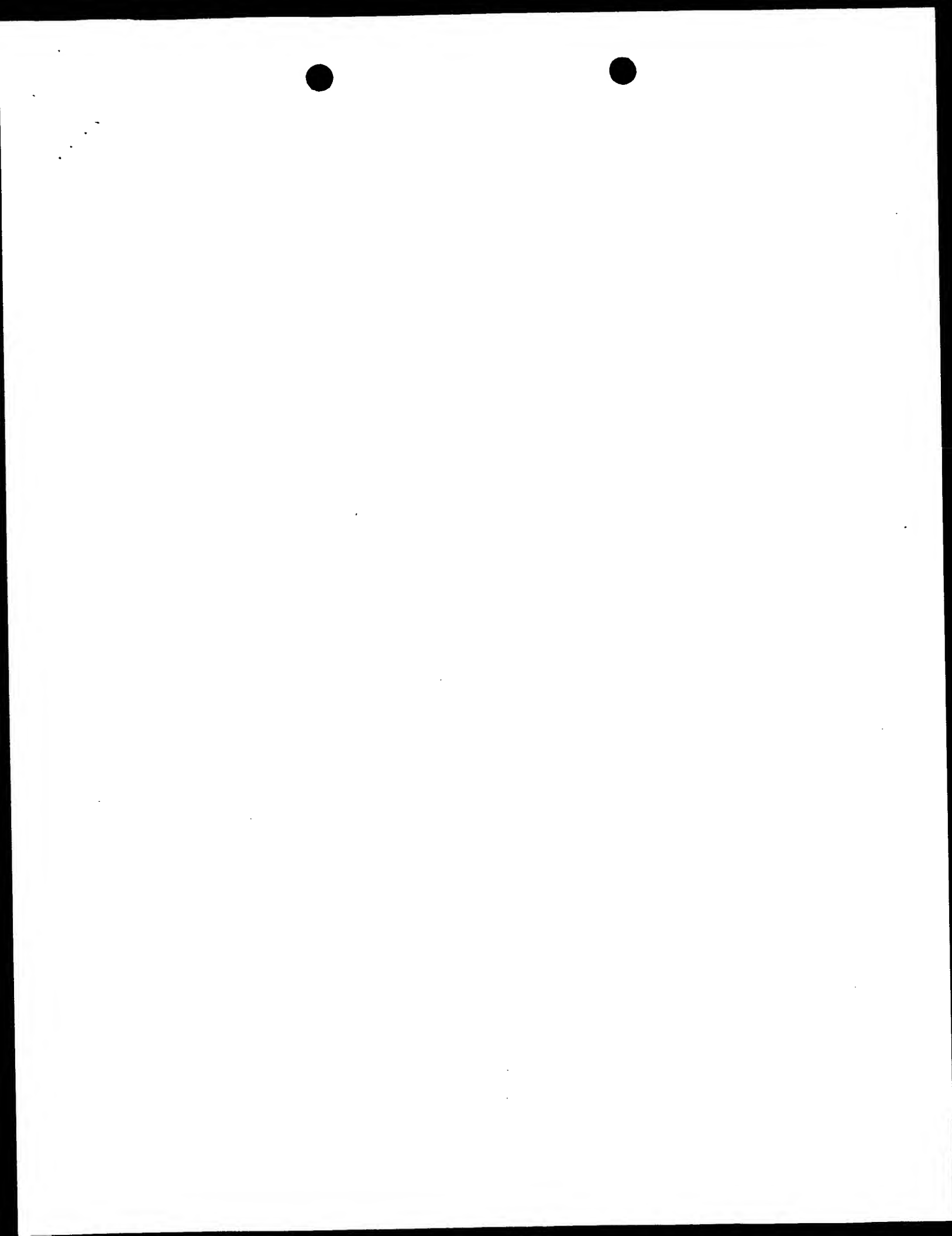
XX Location/Qualifiers

FT Peptide 1..21 /label= Signal-peptide  
 FT Protein 22..249 /label= DCRS4.1  
 FT /note= "Human mature DNAX cytokine receptor subunit 4.1"  
 FT Modified-site 24 /note= "CK2 phosphorylation site"  
 FT Modified-site 25 /note= "Calcium phosphorylation site"  
 FT Modified-site 28 /note= "PKC phosphorylation site"  
 FT Domain 31..70 /label= Cytokine\_receptor\_domain  
 FT Modified-site 51 /note= "cAMP PK site"  
 FT Modified-site 56 /note= "N-glycosylated"  
 FT Disulfide-bond 78..86 /label= Conserved\_disulphide\_linkage  
 FT Modified-site 81 /note= "Calcium phosphorylation site"  
 FT Modified-site 85 /note= "Calcium phosphorylation site"  
 FT Modified-site 89 /note= "Calcium phosphorylation site"  
 FT Modified-site 92 /note= "Calcium phosphorylation site"  
 FT Modified-site 100 /note= "Amidation site"  
 FT Modified-site 110 /note= "Myristoyl site"  
 FT Modified-site 118 /note= "PKC phosphorylation site"  
 FT Modified-site 119 /note= "cAMP phosphorylation site"  
 FT Modified-site 119 /note= "cAMP PK site"  
 FT Modified-site 124 /note= "Myristoyl site"  
 FT Modified-site 127 /note= "cAMP PK site"  
 FT Modified-site 152 /note= "N-glycosylated"  
 FT Modified-site 157 /note= "N-glycosylated"  
 FT Modified-site 177 /note= "cAMP PK site"  
 FT Modified-site 178 /note= "N-glycosylated"  
 FT Modified-site 180 /note= "Calcium phosphorylation site"  
 FT Modified-site 180 /note= "CK2 phosphorylation site"  
 FT Modified-site 195 /note= "N-glycosylated"  
 FT Modified-site 197 /note= "Calcium phosphorylation site"  
 FT Modified-site 207 /note= "Myristoyl site"  
 FT Modified-site 238 /note= "PKC phosphorylation site"  
 FT Modified-site 241 /note= "Calcium phosphorylation site"  
 XX WO200136467-A2.  
 XX 25-MAY-2001.  
 XX 16-NOV-2000; 2000WO-US31363.  
 XX 18-NOV-1999; 99US-0443060.  
 PR 13-DEC-1999; 99US-0170320.

XX PA (SCHE ) SCHERING CORP.  
 XX Gorman DM;  
 XX WPI; 2001-343800/36.  
 DR N-PSDB; AAD06410.  
 XX New mammalian receptor proteins related to cytokine receptors, useful for regulating cell development and for diagnosis and treatment of immunological disorders  
 XX Claim 3; Page 22; 124pp; English.  
 XX The present sequence is human DNAX cytokine receptor subunit 4.1 (DCRS4.1). DCRS4 gene is located on chromosome 6q24.1-25.2. Cytokine receptors, fragments and antibodies are useful for treating immunological disorders. DCRS3 (50R), DCRS4 (cytor) or fragments are useful in drug screening to identify compounds having binding affinity to the receptor subunit. Modulators of DCRS are useful for modulating the physiology or development of a cell or tissue culture cells. A purified DCRS is useful as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to production of antibody to the endogenous receptor. Cytokine receptor sequences are useful as probes for detecting levels of the cytokine receptor in patients suspected of having an immunological disorder. Antibodies have therapeutic value, are useful as potent antagonist, in detecting or quantifying ligands, for isolating DCRS proteins and peptides, to screen expression libraries for particular expression products, to raise anti-idiotypic antibodies and for detecting or diagnosing various immunological conditions related to expression of the protein or cells which express the protein.  
 XX SQ Sequence 249 AA;  
 Query Match 86.5%; Score 1076; DB 22; Length 249;  
 Best Local Similarity 84.0%; Pred. No. 8.5e-106;  
 Matches 210; Conservative 3; Mismatches 17; Indels 20; Gaps 3;  
 QY 1 MNPKECFGLISFLTGVAGTQSTHESLKPQVQFQSRNFHNLQWQGRALTGNSVY 60  
 DB 1 MNPKECFGLISFLTGVAGTQSTHESLKPQVQFQSRNFHNLQWQGRALTGNSVY 60  
 QY 61 FVOYKIYQORQWKNKEDCWGTQELSCDLTSETSDIQEYVGRVRAASAGSVSEWS----- 115  
 DB 61 FVOYKIYQORQWKNKEDCWGTQELSCDLTSETSDIQEYVGR-RGKNKNGNMPGPKQSK 119  
 QY 116 -----MTPRFTPWNE--TKIDPPVNNITQVNGSLVTLHAPNLPYRYQKEKNV 161  
 DB 120 RKSKGNQKNTVTAPAAKAFAGCAKIDPPVNNITQVNGSLVTLHAPNLPYRYQKEKNV 179  
 QY 162 STEDYVELLYRVFIINNSLEKEQVYEGHRAVETALTPHSSYCVVAEYQPMLEDRSQ 221  
 DB 180 STEDYVELLYRVFIINNSLEKEQVYEGHRAVETALTPHSSYCVVAEYQPMLEDRSQ 239  
 QY 222 RSEERCVEIP 231  
 DB 240 RSEERCVEIP 249  
 RESULT 15  
 AA017380  
 ID AA017380 standard; Protein; 249 AA.  
 XX AC AA017380;  
 XX 08-AUG-2002 (first entry)  
 DT Human cytokine receptor variant 1.  
 XX Human; cytokine receptor; immune disease; psoriasis; cancer; infection;  
 KW rheumatoid arthritis; multiple sclerosis; Crohn's disease;  
 KW ulcerative colitis; transplant rejection; abortion; antipsoriatic;

KW immunosuppressive; antirheumatic; antiarthritic; neuroprotective;  
KW antiinflammatory; antitumor; cytostatic; dermatological;  
KW chromosome 6q24.1-25.2; receptor.  
XX  
OS Homo sapiens.  
XX  
PN EPI191035-A2.  
XX  
PD 27-MAR-2002.  
XX  
PF 24-AUG-2001; 2001EP-0250307.  
XX  
PR 25-SEP-2000; 2000DE-1048626.  
PR 17-NOV-2000; 2000DE-1058907.  
PR 19-DEC-2000; 2000DE-1064906.  
XX  
PA (SCHD) SCHERING AG.  
XX  
PI Weiss B, Sabat R, Assadullah K, Toshi L,  
XX  
DI MPI; 2002-332210/37.  
XX  
DI N-PSDB; AAL45999.  
XX  
PT New nucleic acid encoding soluble cytokine receptor, useful for  
PT diagnosis and treatment of e.g. immune disease, also related protein  
PT and antibodies  
XX  
PS Claim 6; Page 12-13; 21pp; German.  
XX  
CC The present invention provides the protein and coding sequences of 3  
CC variants of a human cytokine receptor. The sequences can be used in the  
CC diagnosis, prevention and treatment of immune diseases, including  
CC psoriasis, cancer, chronic/life-threatening infections, rheumatoid  
CC arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and  
CC transplant rejection and in reproductive medicine, e.g. for diagnosing  
CC abnormal immune reactions which cause abortions. The present sequence is  
CC variant 1 of the invention.  
XX  
SQ Sequence 249 AA;  
  
Query Match 86.5%; Score 1076; DB 23; Length 249;  
Best Local Similarity 84.0%; Pred. No. 8.5e-106;  
Matches 210; Conservative 3; Mismatches 17; Indels 20; Gaps 3;  
  
QY 1 MMRHCHLGLIFLTVAGTOSTHESLKPQVQFQSRNPHNLIOWOPGRALTGNSSVY 60  
DB 1 MMRHCHLGLIFLTVAGTOSTHESLKPQVQFQSRNPHNLIOWOPGRALTGNSSVY 60  
QY 61 FVOYKLYGQROWKNEKDCWGTOLSCDLTSETSDIOEPYGRVRAASAGSYSWS----- 115  
DB 61 FVOYKLYGQROWKNEKDCWGTOLSCDLTSETSDIOEPYGRVRAASAGSYSWS----- 115  
QY 116 -----MTPRFTPMWE--TKIDPPVNNITOVNGSLVITLHAPNLPYRQKENV 161  
DB 120 RSKSGNQKNTNTVAPALAKAFAGCAKIDPPVNNITOVNGSLVITLHAPNLPYRQKENV 179  
QY 162 STEDYVELLYRFFIINNSLEKEQYEGAHRAVEIALTPHSSYCVVAEIQPMLDRSQ 221  
DB 180 STEDYVELLYRFFIINNSLEKEQYEGAHRAVEIALTPHSSYCVVAEIQPMLDRSQ 239  
QY 222 RSEERCVEIP 231  
DB 240 RSEERCVEIP 249

Search completed: January 13, 2003, 15:30:53  
Job time : 32.993 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:31:05 ; Search time 11.3873 Seconds

(without alignments)  
596.865 Million cell updates/sec

Title: US-09-728-911-2

Sequence: 1 MPMKCFGLISFLTGVA.....YQMLDRSQSRSEECVEIP 231

Scoring table: BLOSUM62

Gap: 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: Issued Patents AA:  
1: /cgn2\_6/prodata/1/aa/5A.COMB.pep:\*  
2: /cgn2\_6/prodata/1/aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/1/aa/6A.COMB.pep:\*  
4: /cgn2\_6/prodata/1/aa/6B.COMB.pep:\*  
5: /cgn2\_6/prodata/1/aa/6C.COMB.pep:\*  
6: /cgn2\_6/prodata/1/aa/6D.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	337	27.1	221	2	US-08-943-087-52
2	336	27.0	221	2	US-08-943-087-50
3	336	27.0	221	2	US-08-943-087-56
4	336	27.0	221	2	US-08-943-087-52
5	336	27.0	221	2	US-08-943-087-52
6	336	27.0	221	2	US-08-943-087-16
7	336	27.0	221	2	US-08-943-087-16
8	336	27.0	221	2	US-08-943-087-16
9	336	27.0	221	2	US-08-943-087-16
10	336	27.0	221	2	US-08-943-087-20
11	336	27.0	221	2	US-08-943-087-22
12	336	27.0	221	2	US-08-943-087-24
13	336	27.0	221	2	US-08-943-087-26
14	336	27.0	221	2	US-08-943-087-30
15	336	27.0	221	2	US-08-943-087-32
16	336	27.0	221	2	US-08-943-087-34
17	336	27.0	221	2	US-08-943-087-36
18	336	27.0	221	2	US-08-943-087-38
19	336	27.0	221	2	US-08-943-087-40
20	336	27.0	221	2	US-08-943-087-42
21	336	27.0	221	2	US-08-943-087-44
22	336	27.0	221	2	US-08-943-087-46
23	336	27.0	221	2	US-08-943-087-48
24	336	27.0	221	2	US-08-943-087-50
25	336	27.0	221	2	US-08-943-087-52
26	336	27.0	221	2	US-08-943-087-54
27	336	27.0	221	2	US-08-943-087-56

28	183.5	14.8	575	1	US-08-110-683-4	Sequence 4, Appli
29	183.5	14.8	575	2	US-08-477-166-4	Sequence 4, Appli
30	183.5	14.8	575	2	US-08-472-097-4	Sequence 4, Appli
31	183.5	14.8	575	2	US-08-472-097-4	Sequence 4, Appli
32	183.5	14.8	575	5	PCT-US93-11638-4	Sequence 4, Appli
33	181	14.5	559	1	US-08-424-788-3	Sequence 3, Appli
34	172	13.8	251	1	US-07-882-2028-2	Sequence 3, Appli
35	172	13.8	251	1	US-07-882-2028-2	Sequence 3, Appli
36	172	13.8	251	1	US-07-882-2028-2	Sequence 3, Appli
37	172	13.8	251	1	US-08-021-615A-2	Sequence 2, Appli
38	172	13.8	251	1	US-08-321-777-2	Sequence 2, Appli
39	172	13.8	251	1	US-08-463-931-6	Sequence 2, Appli
40	172	13.8	251	1	US-08-464-237A-4	Sequence 2, Appli
41	172	13.8	251	5	PCT-US92-02888A-4	Sequence 4, Appli
42	172	13.8	251	5	PCT-US93-04933-2	Sequence 4, Appli
43	172	13.8	295	2	US-08-463-931-2	Sequence 2, Appli
44	172	13.8	295	2	US-08-372-887-20	Sequence 2, Appli
45	168.5	13.5	325	2	US-09-224-048A-4	Sequence 4, Appli

## ALIGNMENTS

RESULT 1  
US-08-943-087-52  
Sequence 52, Application US/08943087  
Patent No. 5945511  
GENERAL INFORMATION:  
APPLICANT: Lok, Si  
APPLICANT: Kuo, Choon J.  
APPLICANT: Jernberg, Anna C.  
APPLICANT: Adams, Robyn L.  
APPLICANT: Whitmore, Theodore E.  
TITLE OF INVENTION: CYTOKINE RECEPTOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,087  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/803,305  
FILING DATE: 20-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lunn, Paul G  
REGISTRATION NUMBER: 32,743  
REFERENCE/DOCKET NUMBER: 96-24C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 221 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-943-087-52



Mon Jan 13 15:37:28 2003

Matches 74; Conservative 33; Mismatches 90; Indels 2; Gaps 2;

Query Match 27.1%; Score 337; DB 2; Length 221;  
Best Local Similarity 37.2%; Pred. No. 3.le-29;  
Matches 74; Conservative 33; Mismatches 90; Indels 2; Gaps 2;

QY 30 KPORVQFQRNFHNIOWOPGRALTGNSSVVFQYKIYQORQWKNKEDCWGTQELSCDLT 89  
DB 10 KPGNITFUSIMNKNVLQWTPPEGLOGVKVYTYVQYFIYGQKWLKSECRNINRTYCDLS 69  
QY 90 SETSDIQEPPYGRVRAASAGSYSEWSMTPTPTWETKIDPPVNMNITOVNGSLVILHAP 149  
DB 70 AETSDYEHQYAKVKAIMGTKSKWAESGRFPFLETOIGPPEVGLTTDEKSISSVLTAP 129  
QY 150 NLPYRQKEKNVSIEDY-ELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVW 208  
DB 130 EKWKRNPEDLVSMQOIIYNSLKNVSVLNTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVH 188  
QY 209 AEIYQPMIDRRSRSEERC 227  
DB 189 VESFVGPFPRAQPSKQC 207

RESULT 2

US-08-943-087-50  
; Sequence 50, Application US/08943087  
; Patent No. 5945511  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Kho, Choon J.  
; APPLICANT: Jelmeberg, Anna C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Farrah, Theresa M.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,087  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/803,305  
; FILING DATE: 20-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-24C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 221 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-943-087-50

Query Match 27.0%; Score 336; DB 2; Length 221;  
Best Local Similarity 37.2%; Pred. No. 4e-29;

QY 30 KPORVQFQRNFHNIOWOPGRALTGNSSVVFQYKIYQORQWKNKEDCWGTQELSCDLT 89  
DB 10 KPGNITFUSIMNKNVLQWTPPEGLOGVKVYTYVQYFIYGQKWLKSECRNINRTYCDLS 69  
QY 90 SETSDIQEPPYGRVRAASAGSYSEWSMTPTPTWETKIDPPVNMNITOVNGSLVILHAP 149  
DB 70 AETSDYEHQYAKVKAIMGTKSKWAESGRFPFLETOIGPPEVGLTTDEKSISSVLTAP 129  
QY 150 NLPYRQKEKNVSIEDY-ELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVW 208  
DB 130 EKWKRNPEDLVSMQOIIYNSLKNVSVLNTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVH 188  
QY 209 AEIYQPMIDRRSRSEERC 227  
DB 189 VESFVGPFPRAQPSKQC 207

RESULT 3

US-08-943-087-56  
; Sequence 56, Application US/08943087  
; Patent No. 5945511  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Kho, Choon J.  
; APPLICANT: Jelmeberg, Anna C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Farrah, Theresa M.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,087  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/803,305  
; FILING DATE: 20-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-24C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 221 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-943-087-56

Query Match 27.0%; Score 336; DB 2; Length 221;  
Best Local Similarity 36.7%; Pred. No. 4e-29;  
Matches 73; Conservative 34; Mismatches 90; Indels 2; Gaps 2;

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:28:50 ; Search time 12.743 seconds

(without alignments)  
1742.692 Million cell updates/sec

Title: US-09-728-911-2

Sequence: 1 MMRKHCFLGFLISFLITGVA.....YQPMIDRRSQSRSEECVEIP 231

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1: PIR 73: \*  
2: PIR1: \*  
3: PIR2: \*  
4: PIR3: \*  
5: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	183.5	14.8	575 2 A49667	interleukin-10 rec
2	173	13.9	349 2 JC6311	interferon recepto
3	172	13.8	295 1 KFRH3	tissue factor prec
4	168.5	13.5	325 2 A47003	cytokine receptor
5	165	13.3	560 2 S27387	interferon alpha r
6	159	12.8	578 2 I56215	interleukin-10 rec
7	150.5	12.1	292 1 KFB03	tissue factor prec
8	148.5	11.9	590 2 A45283	interferon alpha/b
9	143.5	11.5	292 1 KFRH3	tissue factor prec
10	143.5	11.5	557 2 A32694	interferon gamma r
11	138.5	11.1	489 2 A31555	tissue factor prec
12	136	10.9	294 1 KFRH3	interferon gamma r
13	114.5	9.2	332 2 A49947	interferon alpha/b
14	110.5	8.9	515 2 I39073	interferon alpha/b
15	108.5	8.7	331 2 A54295	interferon recepto
16	108.5	8.7	331 2 S59501	interferon gamma r
17	107	8.6	337 2 I38500	interferon gamma r
18	98	7.9	477 2 A34368	Kallmann syndrome
19	97.5	7.8	674 2 A47222	Kallmann syndrome
20	97.5	7.8	674 2 B47222	gene B9R protein
21	95	7.6	266 2 I36855	B9R 31k protein pr
22	91	7.3	272 2 J01802	B9R protein - vacc
23	90	7.2	272 2 C42526	IL1 protein - mou
24	89.5	7.2	1028 2 I58164	IL1 protein - mou
25	89.5	7.2	2215 2 T00348	plasmacytoma-asso
26	89	7.1	1028 2 A53449	hypothetical prote
27	88	7.1	266 2 T28607	H9R protein - vari
28	87	7.0	266 2 H72172	acid phosphatase
29	84.5	6.8	464 1 B59200	

30	84	6.8	792 2 S16680	ribonucleoside-dip
31	83.5	6.7	263 2 A44229	interferon-gamma r
32	83	6.7	1259 2 S36126	neural cell adhesi
33	82.5	6.6	478 1 ILECD	hemolysin export s
34	82.5	6.6	564 2 JC7365	sepin-like proteol
35	82	6.6	817 2 A48721	littin, muscle - ch
36	82	6.6	894 2 S50128	glutamate receptor
37	82	6.6	894 2 S53696	glutamate receptor
38	82	6.6	894 2 S49460	glutamate receptor
39	81.5	6.6	1260 1 S05479	neural cell adhesi
40	81	6.5	810 2 E71550	glutamate receptor
41	81	6.5	888 2 C40170	glutamate receptor
42	80.5	6.5	468 1 B84540	glutamate receptor
43	80.5	6.5	478 2 S10058	acid phosphatase
44	80.5	6.5	1019 2 C96519	hemolysin secretio
45	80	6.4	716 1 W2BEB6	probable disease r

## ALIGNMENTS

### RESULT 1

A49667 interleukin-10 receptor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #ext\_change 28-Jul-2000

C:Accession: A49667

R:Ho, A.S.; Liu, Y.; Khan, T.A.; Hsu, D.H.; Bazan, J.F.; Moore, K.W.

Proc. Natl. Acad. Sci. U.S.A. 90, 11267-11271, 1993

A:Title: A receptor for interleukin 10 is related to interferon receptors.

A:Reference number: A49667; PMID:94068585; PMID:8248239

A:Accession: A49667

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-575 <RES>

A:Cross-references: GB:U12120; NID:G437615; PIDN:AAA16156.1; PID:G437615

A:Gene: IL10R

C:Superfamily: Interleukin-10 receptor IL10R

C:Keywords: cytokine receptor

Query Match 14.8%; Score 183.5; DB 2; Length 575;

Best Local Similarity 30.2%; Pred. No. 1e-08;

Matches 74; Conservative 34; Mismatches 92; Indels 45; Gaps 14;

QY 7 FLGLISFLITGVA-GTOSTHESLKQRYQFOSKRNHNLQPGRALTGNSVYFQYK 65

Db 8 FLVTISLSLEFLTAGT---ELPSPSYVWFARFQHLHWKP-IPNQSSTYEVVALK 62

QY 66 IYQGRQKNEKDCWGTQELSCDLTSTSDIQEPYVG---RVRAASAGSYSEMSMT-PRFT 121

Db 63 QYGNSTWNDIHLCKKQALSCDLTFTTDLVHRSYGVARVAUNSOISWMTTETRTFT 122

QY 122 PMWETKIDPPVNAVITQY---NGSLVLTHAPNLPYRQKEKNVSIIDYELLY---RV 173

Db 123 ---VDEVILTVDSVTLKAMDGIYGTIHPB-----RRTTPADDEREQYFKDLR 169

QY 174 FIINSLERKQKYEGCAHVAIEALT-----PHSSYCVAEIYQPMIDR---SONSEE 225

Db 170 YK--SIRKFSEL-KKATGRVQKQETFLTPVIGRKKFCVQ---LPRLESINKAWESEE 223

QY 226 RCVEI 230

Db 224 QCLLI 228

### RESULT 2

JC6311 interferon receptor-class II cytokine receptor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #ext\_change 11-May-2000

C:Accession: JC6311

R:Gibbs, V.C.; Pennica, D.

Gene 186, 97-101, 1997  
A>Title: CRF2-4: Isolation of cDNA clones encoding the human and mouse proteins.  
A/Reference number: JC6311; MUID:97199375; PMID:9047351  
A/Accession: JC6311  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-349 <GIB>  
A/Cross-references: GB:U53596

Query Match 13.9%; Score 173; DB 2; Length 349;  
Best Local Similarity 29.8%; Pred. No. 4.7e-08;  
Matches 70; Conservative 30; Mismatches 93; Indels 42; Gaps 12;

QY 6 CFLGFLISFFLTGAGTQSTHESLKPQVQFQSRNPHNLOQW----PGRALTGNSVYF 61  
DB 4 CVAGWLGGLLPALGMP-----PPEKVRNNSVFNKILQWEPAPFKTNLT-----FT 53

QY 62 VOYKYGQWKNKEDCGTQELSCDLT--SETSDIOEPYIGYGRVRAASAGSYSEWMTFR 119  
DB 54 AQYESYRSFQ---DHCKRTASTQCFSHLSKYGD---YTVRVRAELADEHSEW-VNVT 104

QY 120 FPPWETKIDPPVNMITQVNGSLVILHAPNLPYQKE-----KNVSTEDYELLRYV 173  
DB 105 FCPVEDTIIGPEMQIESLAESLELRFSAPOI-----ENEPETWTLKNI-----YDSWAYRV 156

QY 174 -FLIINLSLEKEQKVEGAHRAVEATLPHSSYCVABEITQPMPLDRRSORSERC 227  
DB 157 QYWKNGTNEKFQV--SPYDSEVLNLEPWTYCIQVQGLLDQNRGTGENSEPIC 209

RESULT 3  
KFH93  
Tissue factor precursor [validated] - human  
N/Alternate names: coagulation factor III  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 08-Dec-2000  
C/Accession: A43645; A47574; A29062; A29062; A29062; A29062  
R/Mackman, N.; Morrissey, J.H.; Fowler, B.; Edgington, T.S.  
Biochemistry 28, 1755-1762, 1989  
A/Title: Complete sequence of the human tissue factor gene, a highly regulated cellular  
A/Reference number: A43645; MUID:89247359; PMID:2719931  
A/Accession: A43645  
A/Molecule type: DNA  
A/Residues: 1-295 <MAC>  
A/Cross-references: GB:J02846; NID:9339505; PIDN:AAA61152.1; PID:9339506  
R/Fisher, K.L.; Gorman, C.M.; Vehar, G.A.; O'Brien, D.P.; Lawn, R.M.  
Thromb. Res. 48, 89-99, 1987  
A/Title: Cloning and expression of human tissue factor cDNA.  
A/Reference number: A47574; MUID:88100453; PMID:3424286  
A/Accession: A47574  
A/Molecule type: mRNA  
A/Residues: 1-295 <PIS>  
A/Cross-references: GB:M27436; NID:9339507; PIDN:AAA36734.1; PID:9339508  
R/Spicer, E.K.; Horton, R.; Bloem, L.; Bach, R.; Williams, K.R.; Guha, A.; Kraus, J.; Li  
Proc. Natl. Acad. Sci. U.S.A. 84, 5148-5152, 1987  
A/Title: Isolation of cDNA clones coding for human tissue factor: primary structure of  
A/Reference number: A94171; MUID:87260946; PMID:3037536  
A/Accession: A28320  
A/Molecule type: mRNA  
A/Residues: 1-295 <SPI>  
A/Cross-references: GB:J02931; NID:9339501; PIDN:AAA61150.1; PID:9339502  
R/Morrissey, J.H.; Fakhrai, H.; Edgington, T.S.  
Cell 50, 129-135, 1987  
A/Title: Molecular cloning of the cDNA for tissue factor, the cellular receptor for the  
A/Reference number: A29062; MUID:87244317; PMID:3297348  
A/Accession: A29062  
A/Molecule type: mRNA  
A/Residues: 1-295 <WOR>  
A/Cross-references: GB:J02931; NID:9339501; PIDN:AAA61150.1; PID:9339502  
R/Scarpati, E.M.; Wen, D.; Broze Jr., G.J.; Miletic, J.P.; Flandermeyer, R.R.; Siegel,  
Biochemistry 26, 5234-5238, 1987  
A/Title: Human tissue factor: cDNA sequence and chromosome localization of the gene.

A/Reference number: A29672; MUID:88050796; PMID:2823875  
A/Accession: A29672  
A/Molecule type: mRNA  
A/Residues: 1-259, 'A', 261-295 <SCA>  
A/Cross-references: GB:M16553; NID:9339503; PIDN:AAA61151.1; PID:9339504  
R/Bach, R.; Konigsberg, W.H.; Nemerson, Y.  
Biochemistry 27, 4227-4231, 1988  
A/Title: Human tissue factor contains thioester-linked palmitate and stearate on the cyto  
A/Reference number: A37422; MUID:8900604; PMID:3166978  
A/Content: annotation; disulfide bonds and fatty acid binding site  
C/Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor  
C/Comment: Expression of tissue factor can be induced in a variety of tissues by certain  
C/Genetics:  
A/Gene: GDB:F3  
A/Cross-references: GDB:119895; OMIM:134390  
A/Map position: 1p22-1p21  
A/Introns: 34/1; 71/2; 138/1; 197/3; 251/1  
C/Superfamily: tissue factor  
C/Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane  
F/1-32/Domain: signal sequence; #status predicted <SIG>  
F/33-295/Product: tissue factor; #status experimental <MAT>  
F/33-251/Domain: extracellular; #status predicted <EXT>  
F/252-274/Domain: transmembrane; #status predicted <TM>  
F/275-295/Domain: intracellular; #status experimental <INT>  
F/43/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F/81-89, 218-241/Disulfide bonds: #status experimental  
F/156, 169/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F/277/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 13.8%; Score 172; DB 1; Length 295;  
Best Local Similarity 25.3%; Pred. No. 4.6e-08;  
Matches 59; Conservative 45; Mismatches 103; Indels 26; Gaps 12;

QY 11 LISFPLTGAGTQSTHESLKPQVQFQSRNPHNLOQWGRALTGNSVYFVQYKIYQQR 70  
DB 21 LLGWFAQVAGAGTNTVAAYNTWKSTNFKTLEWPKPV----NQYTVQIST-KSG 75

QY 71 QWKNKEDCGTQELSCDLTS--TSDIOEPYIGYGRV-----RAASAGSYSE--WSMTPRFT 121  
DB 76 DWKSK--CFYITDTECDLTDIVKDVQVTLARVFSYPAGNVSTGSGEPLYSPEET 133

QY 122 PWEYTKI--DPPVNMITQVNGSLVILHAPNLPYQKEKNVSTEDYV--ELLVYRVFIIN 178  
DB 134 PYLETNLQPTIQSFEQVGTKNVTVDEDTLVR--RNNTFLSLRDVFGKDLITLYYWS 192

QY 179 SLEKEQKVEGAHR--AVEIEALTPHSSYCV--VVAEITQPMPLDRRSORSERCV 228  
DB 193 SSSGKTKTAKTNTNEFLIIVD---KGENYCVSVQAVIPSRVTRNKRKSTDSPEECM 242

RESULT 4  
A47003  
Cytokine receptor family class II protein CRF2-4 precursor - human  
C/Species: Homo sapiens (man)  
C/Date: 09-Sep-1994 #sequence revision 09-Sep-1994 #text change 01-Dec-2000  
C/Accession: A47003; G01418  
R/Lutfalla, G.; Gardiner, K.; Uze, G.  
Genomics 16, 366-373, 1993  
A/Title: A new member of the cytokine receptor gene family maps on chromosome 21 at less  
A/Reference number: A47003; MUID:93300510; PMID:8314576  
A/Accession: A47003  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-325 <LUT>  
A/Cross-references: GB:Z17227; NID:93393378; PIDN:CAA78933.1; PID:9393379  
R/Lutfalla, G.  
submitted to the EMBL Data Library, April 1994  
A/Reference number: G06935  
A/Accession: G01418  
A/Status: preliminary; translated from GB/EMBL/DBD  
A/Molecule type: DNA  
A/Residues: 1-123, 'D', 125-268, 'VGRME' <LUT>  
A/Cross-references: EMBL:U08988; NID:9571295; PID:9571296

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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:28:46 ; Search time 7.0493 seconds

(without alignments)  
1359.147 Million cell updates/sec

Title: US-09-728-911-2

Sequence: 1 MPMKCFGLGFLISFLTGVA.....YQPMIDRRSQSERECVEIP 231

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

T: number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	183.5	14.8	575	110R_MOUSE	Q61727 mus musculu
2	173	13.9	349	110S_MOUSE	Q61190 mus musculu
3	172	13.8	295	1F_HUMAN	P13726 homo sapien
4	168.5	13.5	325	110S_HUMAN	Q08334 homo sapien
5	165	13.3	560	110R_BOVIN	Q04790 bos tauru
6	159	12.8	578	110R_HUMAN	Q13651 homo sapien
7	150.5	12.1	289	1F_CAVPO	Q91188 cavia porce
8	150.5	12.1	292	1F_BOVIN	P30931 bos tauru
9	148.5	11.9	590	110R_MOUSE	P33896 mus musculu
10	144.5	11.6	560	110R_MOUSE	Q28589 ovis aries
11	143.5	11.5	557	1F_RABIT	P24055 oryctolagus
12	143.5	11.5	557	1F_RABIT	P17181 homo sapien
13	142.5	11.5	292	1F_RABIT	P42533 rattus norv
14	138.5	11.1	489	110R_HUMAN	P15260 homo sapien
15	138	11.1	294	1F_MOUSE	P20352 mus musculu
16	123	9.9	536	110R_MOUSE	Q95207 ovis aries
17	119	8.7	530	110R_MOUSE	Q95241 bos tauru
18	108.5	8.6	515	110R_MOUSE	P48551 homo sapien
19	107	8.6	337	110R_HUMAN	P38484 homo sapien
20	98	7.9	477	110R_HUMAN	P15261 mus musculu
21	97.5	7.8	274	110R_MOUSE	P33005 gallus gall
22	96.5	7.8	274	110R_MOUSE	P33005 gallus gall
23	91	7.3	272	110R_MOUSE	P33005 gallus gall
24	90	7.2	272	110R_MOUSE	P33005 gallus gall
25	90	7.2	272	110R_MOUSE	P33005 gallus gall
26	89.5	7.2	2215	110R_MOUSE	Q95209 o sortilin-
27	87.5	7.0	2215	110R_MOUSE	Q95209 o sortilin-
28	86	6.9	2214	110R_MOUSE	Q95209 o sortilin-
29	84	6.8	792	110R_HUMAN	Q92673 h sortilin-
30	83	6.7	1259	110R_HUMAN	P23921 homo sapien
31	82.5	6.6	478	110R_HUMAN	P05695 rattus norv
32	82	6.6	478	110R_HUMAN	P05695 rattus norv
33	81.5	6.6	638	110R_HUMAN	P42263 homo sapien
					P79194 macaca mula

34	81.5	6.6	1260	1	CAML_MOUSE	P11627 mus musculu
35	81.5	6.6	1377	1	NEOI_RAT	P97603 rattus norv
36	81.5	6.6	1493	1	NEOI_MOUSE	P97798 mus musculu
37	81.5	6.6	606	1	2214_HUMAN	Q9159 homo sapien
38	81	6.5	888	1	GLR3_RAT	P19492 rattus norv
39	80.5	6.5	478	1	HLXD_ECOLI	P67739 escherichia
40	80	6.4	716	1	HEPA_HSVB	P28946 equine herp
41	79.5	6.4	401	1	AMPQ_PSYIM	O05465 psychrobact
42	79.5	6.4	1411	1	Y297_HUMAN	O15040 homo sapien
43	79	6.4	680	1	KALM_HUMAN	P23352 homo sapien
44	78.5	6.3	529	1	121R_MOUSE	Q91823 mus musculu
45	78.5	6.3	1461	1	NEOI_HUMAN	Q92859 homo sapien

## ALIGNMENTS

RESULT 1  
ID 110R\_MOUSE STANDARD: PRT: 575 AA.

AC 061727  
DT 15-VUL-1998 (Rel. 36, Created)  
DT 15-VUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Interleukin-10 receptor alpha chain precursor (IL-10R-A) (IL-10R1).  
GN IL10RA OR IL10R.  
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6 X AJ F1; TISSUE=Hematopoietic;  
RX MEDLINE=94068585; PubMed=8248239;

RA Ho A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.;  
RT "A receptor for interleukin 10 is related to interferon receptors."  
RL Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).  
CC -1- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; L12120; AAA16156.1; -  
DR MGD; MGI:96538; IL10ra.  
DR InterPro: IPR000282; Cytok\_receptor\_2.  
KW Receptor; Transmembrane; Glycoprotein; Signal.

FT CHAIN 1 575  
FT DOMAIN 17 241  
FT DOMAIN 242 262  
FT DOMAIN 263 575  
FT DISULFID 204 225  
FT CARBOHYD 50 50  
FT CARBOHYD 66 66  
FT CARBOHYD 113 113  
FT CARBOHYD 182 182  
FT CARBOHYD 238 238  
SQ SEQUENCE 575 AA; 64248 MW; 820B9CD576F868B7 CRC64;

FT INTERLEUKIN-10 RECEPTOR ALPHA CHAIN.  
FT EXTRACELLULAR (POTENTIAL).  
FT CYTOPLASMIC (POTENTIAL).  
FT POTENTIAL.  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CHAIN 1 575  
FT DOMAIN 17 241  
FT DOMAIN 242 262  
FT DOMAIN 263 575  
FT DISULFID 204 225  
FT CARBOHYD 50 50  
FT CARBOHYD 66 66  
FT CARBOHYD 113 113  
FT CARBOHYD 182 182  
FT CARBOHYD 238 238  
SQ SEQUENCE 575 AA; 64248 MW; 820B9CD576F868B7 CRC64;

FT INTERLEUKIN-10 RECEPTOR ALPHA CHAIN.  
FT EXTRACELLULAR (POTENTIAL).  
FT CYTOPLASMIC (POTENTIAL).  
FT POTENTIAL.  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CHAIN 1 575  
FT DOMAIN 17 241  
FT DOMAIN 242 262  
FT DOMAIN 263 575  
FT DISULFID 204 225  
FT CARBOHYD 50 50  
FT CARBOHYD 66 66  
FT CARBOHYD 113 113  
FT CARBOHYD 182 182  
FT CARBOHYD 238 238  
SQ SEQUENCE 575 AA; 64248 MW; 820B9CD576F868B7 CRC64;

FT INTERLEUKIN-10 RECEPTOR ALPHA CHAIN.  
FT EXTRACELLULAR (POTENTIAL).  
FT CYTOPLASMIC (POTENTIAL).  
FT POTENTIAL.  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CHAIN 1 575  
FT DOMAIN 17 241  
FT DOMAIN 242 262  
FT DOMAIN 263 575  
FT DISULFID 204 225  
FT CARBOHYD 50 50  
FT CARBOHYD 66 66  
FT CARBOHYD 113 113  
FT CARBOHYD 182 182  
FT CARBOHYD 238 238  
SQ SEQUENCE 575 AA; 64248 MW; 820B9CD576F868B7 CRC64;

FT INTERLEUKIN-10 RECEPTOR ALPHA CHAIN.  
FT EXTRACELLULAR (POTENTIAL).  
FT CYTOPLASMIC (POTENTIAL).  
FT POTENTIAL.  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CHAIN 1 575  
FT DOMAIN 17 241  
FT DOMAIN 242 262  
FT DOMAIN 263 575  
FT DISULFID 204 225  
FT CARBOHYD 50 50  
FT CARBOHYD 66 66  
FT CARBOHYD 113 113  
FT CARBOHYD 182 182  
FT CARBOHYD 238 238  
SQ SEQUENCE 575 AA; 64248 MW; 820B9CD576F868B7 CRC64;

Mon Jan 13 15:37:32 2003

66 IYGORQWKNKEDCWGTQELSCDLSQTSQTPYQY---RVRAASAGSYSEWSMT-PRFT 121  
 63 QYGNSTWNDIHCRAQALSCDLTFTLDLYHRSYGYRAVRADVNSQVSNWTTTTRFT 122  
 122 PWETKIDPPVNMNITQV---NSGLLVILHAPNLPVRYOKENKNSIEDYELLY---RV 173  
 123 -----VDEVILTVDSTVTKAMDGIIIVGTIHP-----RPTITPAGDEYEQVFXDLRV 169  
 174 FIINNSLEKEQKVEGAHRAVEIEALT-----PHSSYCVVAEIQPMLDRR---SORSEE 225  
 170 YKI--STRKPSL-KNATKRVKQETFTLTVPIGVKECVKV---LPRLESINKAEWSEE 223  
 226 RCVEI 230  
 224 QCLLI 228

RESULT 2  
 ID 110S MOUSE STANDARD; PRT; 349 AA.  
 AC Q61190;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)  
 DE (Cytokine receptor class-II CRF2-4).  
 GN IL10RB OR CRFB4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=971199375; PubMed=9047351;  
 RA Gibbs V.C., Pennica D.;  
 RT "CRF2-4: Isolation of cDNA clones encoding the human and mouse  
 proteins";  
 RL Gene 186:97-101 (1997).  
 RN [2]  
 RP CHARACTERIZATION.  
 RX MEDLINE=98130620; PubMed=9463407;  
 RA Spencer S.D., Di Marco F., Hoolley J., Pitts-Meek S., Bauer M.,  
 RA Ryan A.M., Sordat B., Gibbs V.C., Aguet M.;  
 RT "The orphan receptor CRF2-4 is an essential subunit of the interleukin  
 10 receptor";  
 RL J. Exp. Med. 187:571-578 (1998).  
 CC -!- FUNCTION: RECEPTOR FOR IL-10 AND IL-22. SERVES AS AN ACCESSORY  
 CC CHAIN ESSENTIAL FOR THE ACTIVE IL-10 RECEPTOR COMPLEX AND TO  
 CC INITIATE IL-10-INDUCED SIGNAL TRANSDUCTION EVENTS.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL; U53696; AAC53062.1; -;  
 DR MGD; MGI:109380; 1110-b.  
 DR InterPro; IPR000282; Cytok receptor\_2.  
 DR InterPro; IPR003961; FN\_III.  
 DR SMART; SM00060; FN3; 1.  
 DR Receptor; Transmembrane; Glycoprotein; Signal.  
 KW SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 349 INTERLEUKIN-10 RECEPTOR BETA CHAIN.  
 FT DOMAIN 20 220 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 221 241 POTENTIAL.  
 FT DOMAIN 242 349 CYTOPLASMIC (POTENTIAL).  
 FT

FT DOMAIN 113 205 205  
 FT DISULFID 66 74 74  
 FT DISULFID 188 209 209  
 FT CARBOHYD 49 49 49  
 FT CARBOHYD 102 102 102  
 FT CARBOHYD 161 161 161  
 FT CARBOHYD 199 199 199  
 SQ SEQUENCE 349 AA; 39774 MW; 58B4F6B86330A39 CRC64;  
 Query Match 13.9%; Score 173; DB 1; Length 349;  
 Best Local Similarity 29.8%; Pred. No. 9.7e-09;  
 Matches 70; Conservative 30; Mismatches 93; Indels 42; Gaps 12;  
 QY 6 CFLGLISFFLTGVAGTOSTHESLKPQVQSFQNRHNILOWQ-----PGRALTGNSSVYF 61  
 Db 4 CVAGMLGGFLLVPALGMIP-----PPEKVRMNSVNFKNILQWEPVAFPKTTLT-----FT 53  
 QY 62 VOYKIYQGWKNKEDCWGTQELSCDLT--SETSIDIQPPYGRVRAASAGSYSEWSMTPR 119  
 Db 54 AQYESYRSFQ-----DHCKRTASTQCDQFSLSKYGD-----YTVRVAELADEHSEW-VNVT 104  
 QY 120 FTPWMETKIDPPVNMNITQVNSGLLVILHAPNLPVRYOKE-----KNVSIEDYELLYRV 173  
 Db 105 FCPVEDTIIGPPEMQIESLAESLHLRFSAPOI-----ENEPEPTWTLKNI-----YDSWAYRV 156  
 QY 174 -FIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVVAEIQPMLDRRSEERC 227  
 Db 157 QYWKNGTNEKQVQV--SPYDSEVLNLEPWTTCIQVQGLLDQNRGTGEWSEPIC 209

RESULT 3  
 ID TF HUMAN STANDARD; PRT; 295 AA.  
 AC P13726;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tissue factor precursor (TF) (Coagulation factor III)  
 DE (Thromboplastin) (CD142 antigen).  
 GN F3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89247339; PubMed=2719931;  
 RA Mackman N., Morrissey J.H., Fowler B., Edgington T.S.;  
 RT "Complete sequence of the human tissue factor gene, a highly  
 RT regulated cellular receptor that initiates the coagulation protease  
 RT cascade";  
 RL Biochemistry 28:1755-1762 (1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87260946; PubMed=3037536;  
 RA Spicer E.K., Horton R., Bloem L., Bach R., Williams K.R., Guha A.,  
 RA Kraus J., Lin T.C., Nemerson Y., Konigsberg W.H.;  
 RT "Isolation of cDNA clones coding for human tissue factor: primary  
 RT structure of the protein and cDNA".  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5148-5152 (1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87244317; PubMed=3297348;  
 RA Morrissey J.H., Fakhrai H., Edgington T.S.;  
 RT "Molecular cloning of the cDNA for tissue factor, the cellular  
 RT receptor for the initiation of the coagulation protease cascade";  
 RL Cell 50:129-135 (1987).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88050796; PubMed=2823875;  
 RA Scarpati E.M., Wen D., Broze G.J. Jr., Milewich J.P.,  
 RA Pflandermeyer R.R., Siegel N.R., Sadler J.E.;  
 RT "Human tissue factor: cDNA sequence and chromosome localization of

110S MOUSE STANDARD; PRT; 349 AA.  
 ID 110S MOUSE STANDARD; PRT; 349 AA.  
 AC Q61190;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)  
 DE (Cytokine receptor class-II CRF2-4).  
 GN IL10RB OR CRFB4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=971199375; PubMed=9047351;  
 RA Gibbs V.C., Pennica D.;  
 RT "CRF2-4: Isolation of cDNA clones encoding the human and mouse  
 proteins";  
 RL Gene 186:97-101 (1997).  
 RN [2]  
 RP CHARACTERIZATION.  
 RX MEDLINE=98130620; PubMed=9463407;  
 RA Spencer S.D., Di Marco F., Hoolley J., Pitts-Meek S., Bauer M.,  
 RA Ryan A.M., Sordat B., Gibbs V.C., Aguet M.;  
 RT "The orphan receptor CRF2-4 is an essential subunit of the interleukin  
 10 receptor";  
 RL J. Exp. Med. 187:571-578 (1998).  
 CC -!- FUNCTION: RECEPTOR FOR IL-10 AND IL-22. SERVES AS AN ACCESSORY  
 CC CHAIN ESSENTIAL FOR THE ACTIVE IL-10 RECEPTOR COMPLEX AND TO  
 CC INITIATE IL-10-INDUCED SIGNAL TRANSDUCTION EVENTS.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
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 CC EMBL; U53696; AAC53062.1; -;  
 DR MGD; MGI:109380; 1110-b.  
 DR InterPro; IPR000282; Cytok receptor\_2.  
 DR InterPro; IPR003961; FN\_III.  
 DR SMART; SM00060; FN3; 1.  
 DR Receptor; Transmembrane; Glycoprotein; Signal.  
 KW SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 349 INTERLEUKIN-10 RECEPTOR BETA CHAIN.  
 FT DOMAIN 20 220 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 221 241 POTENTIAL.  
 FT DOMAIN 242 349 CYTOPLASMIC (POTENTIAL).  
 FT

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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:28:46 ; Search time 26.0282 Seconds

(without alignments)  
1828.668 Million cell updates/sec

Title: US-09-728-911-2

Perfect score: 1244  
Sequence: 1 MPMKCFGLGFLISFLTGVA.....YQPMIDRRSQRSERCEVIEIP 231

Scoring table: BLOSUM62

Gappop 10.0 , Gapept 0.5

Searched: 671580 seqs, 206047115 residues

T number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SP\_ARCHAEA:.\*  
2: SP\_BACTERIA:.\*  
3: SP\_FUNGI:.\*  
4: SP\_HUMAN:.\*  
5: SP\_INVERTEBRATE:.\*  
6: SP\_MAMMAL:.\*  
7: SP\_MHC:.\*  
8: SP\_ORGANELLE:.\*  
9: SP\_PHAGE:.\*  
10: SP\_PLANT:.\*  
11: SP RODENT:.\*  
12: SP\_VIRUS:.\*  
13: SP\_VERTEBRATE:.\*  
14: SP\_UNCLASSIFIED:.\*  
15: SP\_VIRUS:.\*  
16: SP\_BACTERIAP:.\*  
17: SP\_ARCHAEP:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1244	100.0	231	4	096A41
2	1218	97.9	263	4	096A05
3	695	55.9	130	4	096GRO
4	336	27.0	553	4	096HFA
5	336	27.0	553	4	096SH8
6	288	23.2	209	4	096SH7
7	266	21.4	574	4	096H22
8	210.5	16.9	569	11	096ND6
9	193.5	15.6	294	13	096W13
10	189.5	15.2	341	13	096Y08
11	168.5	13.5	325	4	096BU4
12	166	13.3	351	11	096VM7
13	160	12.9	442	13	096VJ9
14	158	12.7	569	13	096VJ9
15	143.5	11.5	557	4	08W722
16	140	11.3	294	11	08R3Q1

17	138.5	11.1	332	6	096K86	096K86 ovis aries
18	136.5	11.0	489	4	096Y69	096Y69 homo sapien
19	127.5	10.2	508	13	096YV9	096YV9 gallus gall
20	125.5	10.1	508	13	096VW0	096VW0 gallus gall
21	124	10.0	484	4	014936	014936 homo sapien
22	114.5	9.2	332	11	063953	063953 mus musculu
23	108.5	8.7	239	4	015467	015467 homo sapien
24	108.5	8.7	331	4	096U40	096U40 homo sapien
25	98.5	7.9	608	6	096U07	096U07 monodelphis
26	98	7.9	477	11	091Y85	091Y85 mus musculu
27	97.5	7.8	674	13	090369	090369 gallus gall
28	97.5	7.8	675	13	096SH7	096SH7 rattus norv
29	97	7.8	464	11	096QZ2	096QZ2 rattus norv
30	95.5	7.7	2959	11	090JF1	090JF1 rattus norv
31	95	7.6	266	12	089190	089190 variola vir
32	95	7.6	266	12	066793	066793 ectromelia
33	93.5	7.5	1289	4	09Y2A5	09Y2A5 homo sapien
34	93	7.5	271	12	072744	072744 cowpox viru
35	92.5	7.4	1155	17	081E03	081E03 cowpox viru
36	92.5	7.4	351	17	081E07	081E07 methanosarc
37	91.5	7.3	266	12	08V2J5	08V2J5 vaccinia vi
38	91	7.3	272	12	09JF43	09JF43 vaccinia vi
39	91	7.3	389	13	096E23	096E23 xenopus lae
40	91	7.3	442	13	096E22	096E22 xenopus lae
41	91	7.2	848	2	09K1B4	09K1B4 porphyromon
42	90	7.2	1028	11	062682	062682 rattus norv
43	89	7.2	1028	11	007409	007409 mus musculu
44	89	7.2	266	12	089543	089543 variola vir
45	88	7.1				

## ALIGNMENTS

RESULT 1  
Q6A41 PRELIMINARY; PRT; 231 AA.

AC 096A41;  
DT 01-DEC-2001 (TREMURel. 19, Created)  
DT 01-DEC-2001 (TREMURel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMURel. 20, Last annotation update)  
DE Soluble cytokine class II receptor, short isoform precursor  
DE (Interleukin-22-binding protein CRF2-10) (Class II cytokine receptor)  
DE CRF2-S1 OR IL22BP OR IL22RA2 OR IL-22BP.  
GN Homo sapiens (human)  
OS Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=MAMMARY GLAND;  
RX MEDLINE=21518574; PubMed=11607789;  
RA Gruenberg B.H., Schoenmeyer A., Weiss B., Toschi L., Kunz S.,  
RT Volk K., Asadullah K., Sabat R.;  
RT "A novel, soluble homologue of the human IL-10 receptor with  
RT preferential expression in placenta.";  
RL Genes Immun. 2:329-334(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21286453; PubMed=11390454;  
RA Kotenko S.V., Izotova L.S., Mironchukchenko O.V., Esterova E.,  
RT Katsenhebe H., Donnelly R.P., Pestka S.;  
RT "Identification, cloning, and characterization of a novel soluble  
RT receptor that binds IL-22 and neutralizes its activity.";  
RN J. Immunol. 166:7096-7103(2001).  
RP SEQUENCE FROM N.A.  
RX MEDLINE=2196522; PubMed=11481447;  
RA Xu W., Preneil S.R., Parrish-Novak J., Kindsvogel W., Jaspers S.,  
RT Chen Z., Dillon S.R., Gao Z., Gilbert T., Madden K., Schlutsmeyer S.,  
RA Yao L., Whitmore T.E., Chandrasekhar Y., Grant F.J., Maurer M.,  
RA Jelinek L., Storey H., Brender T., Hammond A., Topouzis S.,

RA Clegg C.H., Foster D.C.;  
 RT "A soluble class II cytokine receptor, IL-22RA2, is a naturally  
 RT occurring IL-22 agonist.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9511-9516(2001).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BBREAST;  
 RA Dumoutier L., Lejeune D., Renaud J.C.;  
 RT "Cloning and characterization of Interleukin-22 Binding Protein (IL-  
 RT 22BP), a natural antagonist of IL-11F/IL-22.";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ313161; CAC85634.1; -;  
 DR EMBL: AY040566; AAK85714.1; -;  
 DR EMBL: AY044429; AAK91775.1; -;  
 DR EMBL: AJ297282; CAC83097.1; -;  
 DR InterPro; IPR000282; Cytok\_receptor\_2.  
 KW Receptor; Signal.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 231 SOLUBLE CYTOKINE CLASS II RECEPTOR, SHORT  
 FT ISOFORM.  
 SQ SEQUENCE 231 AA; 26979 MW; 24A6912BFF75100F CRC64;  
 Query Match 100.0%; Score 1244; DB 4; Length 231;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-111;  
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNPKHCFLGLISFLLTGAGTQSTHESLKPORVQFQSRNFHNLQWPGRALTGNSVY 60  
 DB 1 MNPKHCFLGLISFLLTGAGTQSTHESLKPORVQFQSRNFHNLQWPGRALTGNSVY 60  
 QY 61 FVQYKIYQGRQWKNKEDCWGTQELSCDLTSETSDIQEPIYGRVRAASAGSYSEWMTPRF 120  
 DB 61 FVQYKIYQGRQWKNKEDCWGTQELSCDLTSETSDIQEPIYGRVRAASAGSYSEWMTPRF 120  
 QY 121 TPWETKIDPPVNMNITQVNGSLVLHAPNLPYRQKKNVSIEDYELLVRFVFIINSL 180  
 DB 121 TPWETKIDPPVNMNITQVNGSLVLHAPNLPYRQKKNVSIEDYELLVRFVFIINSL 180  
 QY 181 EKEQYKVEGAHRAVEALTPHSSYCVVAEIQPMLDRRSORSEERCVIEP 231  
 DB 181 EKEQYKVEGAHRAVEALTPHSSYCVVAEIQPMLDRRSORSEERCVIEP 231  
 RESULT 2  
 ID Q969J5 PRELIMINARY; PRT; 263 AA.  
 AC Q969J5; PubMed=11607789;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Soluble cytokine class II receptor, long isoform precursor  
 DE (Interleukin 22-binding protein CRP2-10L).  
 GN CRP2-S1 OR IL22BP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA;  
 RA Gruenberg B.H., Schoenemeyer A., Weiss B., Toschi L., Kunz S.,  
 RA Wolk K., Asadullah K., Sabat R.;  
 RT "A novel, soluble homologue of the human IL-10 receptor with  
 RT preferential expression in placenta.";  
 RL Genes Immun. 2:329-334(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=21286453; PubMed=11390454;  
 RA Kotenko S.V., Izotova L.S., Mirochnitchenko O.V., Esterova E.,  
 RA Dickensheets H., Donnelly R.P., Pestka S.;  
 RT "Identification, cloning, and characterization of a novel soluble  
 RT receptor that binds IL-22 and neutralizes its activity.";  
 RL J. Immunol. 166:7096-7103(2001).  
 DR EMBL: AY040568; AAK85716.1; -;  
 DR InterPro; IPR000282; Cytok\_receptor\_2.  
 SQ SEQUENCE 130 AA; 15128 MW; A165814C641F5E5B CRC64;  
 Query Match 55.9%; Score 695; DB 4; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-59;  
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNPKHCFLGLISFLLTGAGTQSTHESLKPORVQFQSRNFHNLQWPGRALTGNSVY 60  
 DB 1 MNPKHCFLGLISFLLTGAGTQSTHESLKPORVQFQSRNFHNLQWPGRALTGNSVY 60  
 QY 61 FVQYKIYQGRQWKNKEDCWGTQELSCDLTSETSDIQEPIYGRVRAASAGSYSEWMTPRF 120  
 DB 61 FVQYKIYQGRQWKNKEDCWGTQELSCDLTSETSDIQEPIYGRVRAASAGSYSEWMTPRF 120  
 QY 121 TPWE 125

RL J. Immunol. 166:7096-7103(2001).  
 DR EMBL: AJ313162; CAC85635.1; -;  
 DR EMBL: AY040567; AAK85715.1; -;  
 DR InterPro; IPR000282; Cytok\_receptor\_2.  
 KW Receptor; Signal.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 263 SOLUBLE CYTOKINE CLASS II RECEPTOR, LONG  
 FT ISOFORM.  
 SQ SEQUENCE 263 AA; 30550 MW; C96CECE5D78AC79B CRC64;  
 Query Match 97.9%; Score 1218; DB 4; Length 263;  
 Best Local Similarity 87.8%; Pred. No. 8.8e-109;  
 Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;  
 QY 1 MNPKHCFLGLISFLLTGAGTQSTHESLKPORVQFQSRNFHNLQWPGRALTGNSVY 60  
 DB 1 MNPKHCFLGLISFLLTGAGTQSTHESLKPORVQFQSRNFHNLQWPGRALTGNSVY 60  
 QY 61 FVQYKI- YQGRQWKNKEDCWGTQELSCDL 88  
 DB 61 FVQYKIMFSCSMKSHQKPSGCGWHISCNFPCCRTLAKYQGRQWKNKEDCWGTQELSCDL 120  
 QY 89 TSETSDIQEPIYGRVRAASAGSYSEWMTPRFTPWETKIDPPVNMNITQVNGSLVLH 148  
 DB 121 TSETSDIQEPIYGRVRAASAGSYSEWMTPRFTPWETKIDPPVNMNITQVNGSLVLH 180  
 QY 149 PNLPIYQKKNVSIEDYELLVRFVFIINSLKESQKVEGAHRAVEALTPHSSYCVV 208  
 DB 181 PNLPIYQKKNVSIEDYELLVRFVFIINSLKESQKVEGAHRAVEALTPHSSYCVV 240  
 QY 209 AEIYQPMMLDRRSORSEERCVIEP 231  
 DB 241 AEIYQPMMLDRRSORSEERCVIEP 263  
 RESULT 3  
 ID Q96QRO PRELIMINARY; PRT; 130 AA.  
 AC Q96QRO; PubMed=11390454;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Interleukin 22-binding protein CRP2-10S.  
 GN IL22BP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=21286453; PubMed=11390454;  
 RA Kotenko S.V., Izotova L.S., Mirochnitchenko O.V., Esterova E.,  
 RA Dickensheets H., Donnelly R.P., Pestka S.;  
 RT "Identification, cloning, and characterization of a novel soluble  
 RT receptor that binds IL-22 and neutralizes its activity.";  
 RL J. Immunol. 166:7096-7103(2001).  
 DR EMBL: AY040568; AAK85716.1; -;  
 DR InterPro; IPR000282; Cytok\_receptor\_2.  
 SQ SEQUENCE 130 AA; 15128 MW; A165814C641F5E5B CRC64;  
 Query Match 55.9%; Score 695; DB 4; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-59;  
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNPKHCFLGLISFLLTGAGTQSTHESLKPORVQFQSRNFHNLQWPGRALTGNSVY 60  
 DB 1 MNPKHCFLGLISFLLTGAGTQSTHESLKPORVQFQSRNFHNLQWPGRALTGNSVY 60  
 QY 61 FVQYKIYQGRQWKNKEDCWGTQELSCDLTSETSDIQEPIYGRVRAASAGSYSEWMTPRF 120  
 DB 61 FVQYKIYQGRQWKNKEDCWGTQELSCDLTSETSDIQEPIYGRVRAASAGSYSEWMTPRF 120  
 QY 121 TPWE 125



Db 121 TFWME 125

## RESULT 4

ID 09UH4 PRELIMINARY; PRT; 553 AA.

AC 09UH4: 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 GN Class II cytokine receptor ZCYTOR7.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lok S., Kho C., Jelmberg A., Adams R., Whitmore T., Farrah T.,  
 R. O'Hara P.  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,  
 RA Martinez T., Hoffman R., O'Hara P.  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF184971; AAF01320.1; -  
 DR HSP: P13726; 2HFT.  
 DR InterPro: IPR000282; Cytok\_receptor\_2.  
 DR InterPro: IPR001187; Tissue\_factor.  
 DR Pfam: PF01108; Tissue\_fac; 1.  
 KW Receptor.  
 SQ SEQUENCE 553 AA; 62533 MW; 7C23C8543B114659 CRC64;

Query Match 27.0%; Score 336; DB 4; Length 553;

Best Local Similarity 37.2%; Pred. No. 9.1e-24;

Matches 74; Conservative 33; Mismatches 90; Indels 2; Gaps 2;

QY 30 KPOVQFOSRNFHNILOMOPGRALITGNSSVFYQYKIYQGRQWKKEGDCWGTQELSCDUT 89  
 DB 39 KPNITFLSINMKNVLOMTPEGLQGVKTYVYFYIYQKMKLNKSECRNINRTYCDLS 98  
 QY 90 SETSDIEPIYGRVRAASAGSYSEMSMTPTPTWETKIDPPVMNITQVNSLVIILHAP 149  
 DB 99 AETSDYEHQYAKVKAIWGTCKSKMAESGRFPLETOIGPEVALITDEXSISVLTAP 158  
 C 150 NLPYQKEKNVSIIDY-ELLYRFTIINNSLEKQKYEGAHRAVEIEALTPHSSYCV 208  
 DB 159 EKKRNPELIPVSMQIYISNLKINVSILNTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVH 217  
 QY 209 AEIYQPMIDRRSQRSERC 227  
 DB 218 VESFVPGPPRRAQPSKQC 236

## RESULT 5

ID 096SH8 PRELIMINARY; PRT; 553 AA.

AC 096SH8: 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE BA204P2.1.1 (interleukin 20 receptor alpha, isoform 1).  
 GN IL20RA.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Griffiths C.;

RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL135902; CAC38375.1; -  
 DR InterPro: IPR000282; Cytok\_receptor\_2.  
 DR InterPro: IPR003961; RN\_III.  
 DR InterPro: IPR001187; Tissue\_factor.  
 DR Pfam: PF01108; Tissue\_fac; 1.  
 DR SMART: SM00060; FN3; 1.  
 KW Receptor.  
 SQ SEQUENCE 553 AA; 62485 MW; D5C2621FDC848328 CRC64;

Query Match 27.0%; Score 336; DB 4; Length 553;

Best Local Similarity 37.2%; Pred. No. 9.1e-24;

Matches 74; Conservative 33; Mismatches 90; Indels 2; Gaps 2;

QY 30 KPOVQFOSRNFHNILOMOPGRALITGNSSVFYQYKIYQGRQWKKEGDCWGTQELSCDUT 89  
 DB 39 KPNITFLSINMKNVLOMTPEGLQGVKTYVYFYIYQKMKLNKSECRNINRTYCDLS 98  
 QY 90 SETSDIEPIYGRVRAASAGSYSEMSMTPTPTWETKIDPPVMNITQVNSLVIILHAP 149  
 DB 99 AETSDYEHQYAKVKAIWGTCKSKMAESGRFPLETOIGPEVALITDEXSISVLTAP 158  
 QY 150 NLPYQKEKNVSIIDY-ELLYRFTIINNSLEKQKYEGAHRAVEIEALTPHSSYCV 208  
 DB 159 EKKRNPELIPVSMQIYISNLKINVSILNTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVH 217  
 QY 209 AEIYQPMIDRRSQRSERC 227  
 DB 218 VESFVPGPPRRAQPSKQC 236

## RESULT 6

ID 096SH7 PRELIMINARY; PRT; 209 AA.

AC 096SH7: 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE BA204P2.1.3 (interleukin 20 receptor alpha, isoform 3).  
 GN IL20RA.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Griffiths C.;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL135902; CAC38376.1; -  
 DR InterPro: IPR000282; Cytok\_receptor\_2.  
 KW Receptor.  
 SQ SEQUENCE 209 AA; 23616 MW; 467AB77B3840361 CRC64;

Query Match 23.2%; Score 288; DB 4; Length 209;

Best Local Similarity 37.2%; Pred. No. 1.1e-19;

Matches 61; Conservative 29; Mismatches 72; Indels 2; Gaps 2;

QY 30 KPOVQFOSRNFHNILOMOPGRALITGNSSVFYQYKIYQGRQWKKEGDCWGTQELSCDUT 89  
 DB 39 KPNITFLSINMKNVLOMTPEGLQGVKTYVYFYIYQKMKLNKSECRNINRTYCDLS 98  
 QY 90 SETSDIEPIYGRVRAASAGSYSEMSMTPTPTWETKIDPPVMNITQVNSLVIILHAP 149  
 DB 99 AETSDYEHQYAKVKAIWGTCKSKMAESGRFPLETOIGPEVALITDEXSISVLTAP 158  
 QY 150 NLPYQKEKNVSIIDY-ELLYRFTIINNSLEKQKYEGAHRAVEIEALTPHSSYCV 208  
 DB 159 EKKRNPELIPVSMQIYISNLKINVSILNTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVH 217

## RESULT 7

ID 09HB22 PRELIMINARY; PRT; 574 AA.

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AC Q9HB22; 2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE IL-22 receptor.
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=20469498; PubMed=10875937;
RX Xie W.H., Aggarwal S., Ho W.H., Foster J., Zhang Z., Stinson J.,
RA Wood W.I., Goddard A.D., Gurney A.L.;
RT "Interleukin (IL)-22, a Novel Human Cytokine That Signals through the
RT Interferon Receptor-related Proteins CRF2-4 and IL-22R.";
RL J. Biol. Chem. 275:31335-31339(2000).
DR EMBL; AF286095; AAG22073.1; -
DR HSP; P13726; ITH.
DR InterPro; IPR000282; Cytok_receptor_2.
KW Receptor.
SQ SEQUENCE 574 AA; 62977 MW; C179C7085C6F3420 CRC64;

Query Match 21.4%; Score 266; DB 4; Length 574;
Best Local Similarity 33.0%; Pred. No. 4.9e-17;
Matches 69; Conservative 31; Mismatches 93; Indels 16; Gaps 5;

QY 21 GTOSTHSLKP-----ORVQFQSRNHNILQWQGRALTGNSVYVQYKIQGRQWKNKE 76
DB 11 GSUAHAPEPSLLQHVKEQSSNFENILTWDSGPGTDP-TVYIEYKTYGERDWAOK 69
QY 77 DCMGTQELSCDLTSETSDIQEYVYGRVRAASAGSYSEWSMTFRFTPMWETKIDPPVMNIT 136
DB 70 GCQIRTKSCNLTVECTGNLTLYYARVAVSAGRSATKMTDRFSLQTLTKPPDVTCI 129
QY 137 QVNGSLVILHAPNLPVRYQKKNVSTED-YVELLYRVFTINNSLEKEQKVE-----GAH 191
DB 130 SKVRSIQMIVHPTPTTPRAGDGHRLTLEDIFDLFYHLEQVN-----RTYQMHLLGGK 183
QY 192 RAVIEALTPHSSYCVVAEIQPMLDRS 220
DB 184 REYFFGLTPTDTEFLGTIMICVPTWAKES 212

RESULT 8
Q99ND6 PRELIMINARY; PRT; 569 AA.
AC Q99ND6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Interleukin-10 receptor, alpha chain precursor.
GN IL-10RA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RP TISSUE=PERIPHERAL BLOOD;
RC Ward H., Vigness S., Poole S., Bristow A.F.;
RA Ward H., Vigness S., Poole S., Bristow A.F.;
RT "The rat interleukin-10 receptor: cloning and sequencing of cDNA
RT coding for the alpha-chain protein sequence, and demonstration by
RT western blotting of expression in rat brain.";
RL Cytokine 030-0(0).
DR EMBL; AJ305049; CAC24567.1; -
DR InterPro; IPR000282; Cytok_receptor_2.
KW Receptor.
FT CHAIN 1 16 POTENTIAL.
FT CHAIN 17 569 INTERLEUKIN-10 RECEPTOR.
SQ SEQUENCE 569 AA; 63526 MW; 2354FD61DB351BD2 CRC64;

Query Match 15.6%; Score 193.5; DB 13; Length 294;
Best Local Similarity 29.3%; Pred. No. 2e-10;
Matches 72; Conservative 37; Mismatches 90; Indels 45; Gaps 13;

QY 9 GFLIS--PFLTGVAQTOSTHSLKPQVQFQSRNHNILQWQGRALTGNSVYVQYKI 66
DB 11 GVLLSVLFTTGAAGEDYFPEAMD---VQVSVNNFKTLTWGP-----EPTNYTYVEFSR 63
QY 67 YGQORQWKNKDCWGTQELSCDLTSETSDIQEYVYGRVRAASAGSYSE-----113
DB 64 VGKDRQRNPH-CIRSSRTECDLTNELRNLTQY-----SADLSLPLPGVTSDLVEFP 115
QY 114 WMTPTFTPMWETKIDPPVMNITQVNGSLVILHAPN-LPVRYQKKNVSTEDY--ELL 170
DB 116 YTRAERFSYKHTKIGGPAFKIVQSEDKTKMTLHQDPLTPLYKDDQLLTIRDFKSLDK 175
QY 171 YRVFTIN--NSLEKEQKVEGAHRAVEIEALTPHSSYCVVAEIQPMLDRRSQR-----S 223
DB 17 YRVFTIN--NSLEKEQKVEGAHRAVEIEALTPHSSYCVVAEIQPMLDRRSQR-----S 223

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